

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2004, 10:03:28 ; Search time 16.5 Seconds
(without alignments)
137.669 Million cell updates/sec

Title: SEQ1-4SUBS

Perfect score: 1 ANSFLXXLRGSLRXICIXX.....XXAKIFEDVDTLAFWSKH 44

Sequence: BLOSUM62

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/6C.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/6D.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARYS

Result No.	Score	Query Match Length	ID	Description
1	179	90.9	44	US-08-955-636-24
2	179	90.9	419	US-10-182-263-6
3	176	89.3	44	US-08-955-636-35
4	174	88.3	419	US-10-182-263-3
5	174	88.3	419	US-10-182-263-4
6	174	88.3	419	US-10-182-263-5
7	173	87.8	44	US-08-955-636-20
8	170	86.3	44	US-08-955-636-21
9	168	85.3	44	US-08-955-636-19
10	168	85.3	44	US-08-955-636-22
11	160	81.2	44	US-08-955-636-1
12	160	81.2	44	US-08-955-636-25
13	160	81.2	45	US-08-955-636-2
14	160	81.2	419	US-08-955-411-1
15	160	81.2	419	US-08-955-411-1
16	160	81.2	419	US-09-667-570A-3
17	160	81.2	419	US-10-182-263-1
18	160	81.2	419	US-10-182-263-2
19	160	81.2	419	US-10-182-263-3
20	160	81.2	419	US-10-182-263-4
21	160	81.2	419	US-10-182-263-5
22	160	81.2	419	US-10-182-263-6
23	160	81.2	419	US-10-182-263-7
24	160	81.2	419	US-10-182-263-8
25	160	81.2	419	US-10-182-263-9
26	160	81.2	419	US-10-182-263-10
27	160	81.2	419	US-10-182-263-11

28	160	81.2	461	5270178-18	Patent No. 5270178
29	160	81.2	461	5460953-3	Patent No. 5460953
30	147	74.6	42	US-08-745-254A-2	Sequence 2, Appl.1
31	147	74.6	461	5270178-2	Patent No. 5270178
32	143	72.6	41	US-08-229-280-5	Sequence 5, Appl.1
33	138	70.1	42	US-09-383-667-8	Sequence 8, Appl.1
34	129	65.5	409	US-09-065-872-2	Sequence 2, Appl.1
35	129	65.5	409	US-09-667-570A-2	Sequence 1, Appl.1
36	129	65.5	410	US-09-065-872-1	Sequence 1, Appl.1
37	129	65.5	410	US-09-667-570A-1	Sequence 2, Appl.1
38	117	59.4	44	US-08-955-636-23	Sequence 2, Appl.1
39	116	58.9	44	US-08-955-636-2	Sequence 2, Appl.1
40	114	57.9	139	US-08-330-978-2	Sequence 2, Appl.1
41	114	57.9	139	US-08-474-042-2	Sequence 2, Appl.1
42	114	57.9	139	US-08-484-558-2	Sequence 2, Appl.1
43	114	57.9	139	US-08-774-592-2	Sequence 2, Appl.1
44	114	57.9	437	US-08-487-037-2	Sequence 2, Appl.1
45	114	57.9	437	US-08-487-037-3	Sequence 3, Appl.1

ALIGNMENTS

RESULT 1
US-08-955-636-24

Sequence 24, Application US/08955636A

Patent No. 6017882

GENERAL INFORMATION:

APPLICANT: Nelsentuen, Gary

TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT

TITLE OF INVENTION: POLYPEPTIDES

FILE REFERENCE: 09531/002001

CURRENT APPLICATION NUMBER: US/08/955,636A

CURRENT FILING DATE: 1997-10-23

NUMBER OF SEQ ID NOS: 35

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 24

LENGTH: 44

TYPE: PRT

ORGANISM: Homo sapiens

FEATURES:

NAME/KEY: MOD RES

LOCATION: (0)...

OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid

US-08-955-636-24

Query Match 90.9%; Score 179; DB 3; Length 44;

Best Local Similarity 100.0%; Pred. No. 2.1e-23; Indels 0;

Matches 44; Conservative 0; Mismatches 0; Gaps 0;

DB 1 ANSFLXXLRGSLRXICIXXICDPFXAKXIFEDVDTLAFWSKH 44

RESULT 2

US-10-182-263-6

Sequence 6, Application US/10182263

Patent No. 6530138

GENERAL INFORMATION:

APPLICANT: Gerlitz, Bruce E

APPLICANT: Jones, Bryan E

APPLICANT: Grinnell, Brian W

TITLE OF INVENTION: PROTEIN C DERIVATIVES

FILE REFERENCE: X-13611

CURRENT APPLICATION NUMBER: US/10/182,263

CURRENT FILING DATE: 2002-07-22

PRIOR APPLICATION NUMBER: 60/181948

PRIOR FILING DATE: 2002-02-11

PRIOR APPLICATION NUMBER: 60/181948

PRIOR FILING DATE: 2000-03-14

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn version 3.1

SEQ ID NO 6
LENGTH: 419
TYPE: PRT
ORGANISM: Homo sapiens
US-10-182-263-6

Query Match 90.3%; Score 179; DB 4; Length 419;
Best Local Similarity 79.5%; Pred. No. 2, 8e-22;
Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Oy 1 ANSFLXXLRGSLRXCIXXICDPXXAKKIFEDVDTLAFMSKH 44
Db 1 ANSFLXXLRGSLRXCIXXICDPXXAKKIFEDVDTLAFMSKH 44

RESULT 3
US-08-955-636-35
Sequence 35, Application US/08955636A
Patent No. 6017882
GENERAL INFORMATION:
APPLICANT: Nelissen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
FILE REFERENCE: 09531/302001
CURRENT FILING DATE: 1997-10-23
CURRENT APPLICATION NUMBER: US/08/955,636A
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 35
LENGTH: 44
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-35

Query Match 89.3%; Score 176; DB 3; Length 44;
Best Local Similarity 97.7%; Pred. No. 6, 9e-23;
Matches 43; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ANSFLXXLRGSLRXCIXXICDPXXAKKIFEDVDTLAFMSKH 44
Db 1 ANSFLXXLRGSLRXCIXXICDPXXAKKIFEDVDTLAFMSKH 44

RESULT 4
US-10-182-263-3
Sequence 3, Application US/10182263
Patent No. 6630138
GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
APPLICANT: Jones, Bryan E
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: 60/189199
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 419
TYPE: PRT
ORGANISM: Homo sapiens
US-10-182-263-3

Query Match 88.3%; Score 174; DB 4; Length 419;
Best Local Similarity 77.3%; Pred. No. 2e-21;

Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Oy 1 ANSFLXXLRGSLRXCIXXICDPXXAKKIFEDVDTLAFMSKH 44
Db 1 ANSFLXXLRGSLRXCIXXICDPXXAKKIFEDVDTLAFMSKH 44

RESULT 5
US-10-182-263-4
Sequence 4, Application US/10182263
Patent No. 6630138
GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
APPLICANT: Jones, Bryan E
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: 60/189199
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 419
TYPE: PRT
ORGANISM: Homo sapiens
US-10-182-263-4

Query Match 88.3%; Score 174; DB 4; Length 419;
Best Local Similarity 77.3%; Pred. No. 2e-21;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Oy 1 ANSFLXXLRGSLRXCIXXICDPXXAKKIFEDVDTLAFMSKH 44
Db 1 ANSFLXXLRGSLRXCIXXICDPXXAKKIFEDVDTLAFMSKH 44

RESULT 6
US-10-182-263-5
Sequence 5, Application US/10182263
Patent No. 6630138
GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
APPLICANT: Jones, Bryan E
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: 60/189199
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 419
TYPE: PRT
ORGANISM: Homo sapiens
US-10-182-263-5

Query Match 88.3%; Score 174; DB 4; Length 419;
Best Local Similarity 77.3%; Pred. No. 2e-21;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Oy 1 ANSFLXXLRGSLRXCIXXICDPXXAKKIFEDVDTLAFMSKH 44
Db 1 ANSFLXXLRGSLRXCIXXICDPXXAKKIFEDVDTLAFMSKH 44

RESULT 7
US-08-955-636-20
; Sequence 20, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelisestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-20

Query Match 87.8%; Score 173; DB 3; Length 44;
Best Local Similarity 97.7%; Pred. No. 2,2e-22;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ANSFLXLRQGSILRXKXICIXXICDPXXAKXIFEDVDVDTLAFWSKH 44
Db 1 ANSFLXLRQGSILRXKXICIXXICDPXXAKXIFEDVDVDTLAFWSKH 44

RESULT 8
US-08-955-636-21
; Sequence 21, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelisestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-21

Query Match 86.3%; Score 170; DB 3; Length 44;
Best Local Similarity 95.5%; Pred. No. 7,2e-22;
Matches 42; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 ANSFLXLRQGSILRXKXICIXXICDPXXAKXIFEDVDVDTLAFWSKH 44
Db 1 ANSFLXLRQGSILRXKXICIXXICDPXXAKXIFEDVDVDTLAFWSKH 44

RESULT 9
US-08-955-636-19
; Sequence 19, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelisestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531/002001

; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-19

Query Match 85.3%; Score 168; DB 3; Length 44;
Best Local Similarity 95.5%; Pred. No. 1,6e-21;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ANSFLXLRQGSILRXKXICIXXICDPXXAKXIFEDVDVDTLAFWSKH 44
Db 1 ANSFLXLRQGSILRXKXICIXXICDPXXAKXIFEDVDVDTLAFWSKH 44

RESULT 10
US-08-955-636-22
; Sequence 22, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelisestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-22

Query Match 85.3%; Score 168; DB 3; Length 44;
Best Local Similarity 95.5%; Pred. No. 1,6e-21;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ANSFLXLRQGSILRXKXICIXXICDPXXAKXIFEDVDVDTLAFWSKH 44
Db 1 ANSFLXLRQGSILRXKXICIXXICDPXXAKXIFEDVDVDTLAFWSKH 44

RESULT 11
US-08-955-636-1
; Sequence 1, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelisestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

NAME/KEY: MOD_RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-1

Query Match 81.2%; Score 160; DB 3; Length 44;
Best Local Similarity 90.9%; Pred. No. 3.6e-20;
Matches 40; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ANSFLXXLRSGSLRXKICIXXICDPXXAKXIFEDVDPTLAFWSKH 44
DB 1 ANSFLXXLRHSSSLRXKICIXXICDPXXAKXIFQVNDPTLAFWSKH 44

RESULT 12
US-08-955-636-25
Sequence 25, Application US/08955636A
Patent No. 6017882
GENERAL INFORMATION:
APPLICANT: Neisester, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 25
LENGTH: 44
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-25

Query Match 81.2%; Score 160; DB 3; Length 44;
Best Local Similarity 93.2%; Pred. No. 3.6e-20;
Matches 41; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ANSFLXXLRSGSLRXKICIXXICDPXXAKXIFEDVDPTLAFWSKH 44
DB 1 ANSFLXXLRHSSSLRXKICIXXICDPXXAKXIFEDVDPTLAFWSKH 44

RESULT 13
US-08-965-832-2
Sequence 2, Application US/08965832
Patent No. 5847085
GENERAL INFORMATION:
APPLICANT: CHARLES T. ESMON AND MIKHAIL D. SMIRNOV
TITLE OF INVENTION: Modified Protein C
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1201 West
STREET: Peachtree Street
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,832
FILING DATE: 7-NOV-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/745,254

FILING DATE: 8-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/053,768
FILING DATE: 25-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRP 165/167
TELEPHONE: (404)-873-8794
TELEFAX: (404)-873-8795

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

FEATURE:
NAME/KEY:
LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29
OTHER INFORMATION: /note= "where Xaa means gamma
OTHER INFORMATION: carboxyglutamic acid"

NAME/KEY:
LOCATION:
OTHER INFORMATION: /note= "partial sequence of human protein C"

US-08-965-832-2

Query Match 81.2%; Score 160; DB 2; Length 45;
Best Local Similarity 90.9%; Pred. No. 3.7e-20;
Matches 40; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ANSFLXXLRSGSLRXKICIXXICDPXXAKXIFEDVDPTLAFWSKH 44
DB 1 ANSFLXXLRHSSSLRXKICIXXICDPXXAKXIFQVNDPTLAFWSKH 44

RESULT 14
US-08-295-411-1
Sequence 1, Application US/08295411
Patent No. 5679639
GENERAL INFORMATION:
APPLICANT: Griffin, John H.
APPLICANT: Meisters, Rolf M.
TITLE OF INVENTION: Serine protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: For Inhibiting Coagulation
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Office of Patent Counsel, The Scripps
ADDRESSEE: Research Institute
STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/295,411
FILING DATE: 22-AUG-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,989
FILING DATE: 18-NOV-1991
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163

REFERENCE/DOCKET NUMBER: TSRI263.0C1
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Region
LOCATION: 1..157
OTHER INFORMATION: /note= "Protein C Light Chain"
FEATURE:
NAME/KEY: Region
LOCATION: 158..169
OTHER INFORMATION: /note= "Protein C Activation"
OTHER INFORMATION: Peptide
FEATURE:
NAME/KEY: Region
LOCATION: 170..419
OTHER INFORMATION: /note= "Protein C Heavy Chain"
US-08-295-411-1
Query Match
Best Local Similarity 81.2%; Score 160; DB 1; Length 419;
Matches 31; Conservative 2; Mismatches 11; Indels 0; Gaps 0;
Qy 1 ANSFLXLRQSLKXKICIXICDPXKXKIFEDVDTLAFWSK 44
Db 1 ANSFLBELRHSSLERECIEICDFEAKKIFQNVDDTLAFWSK 44
RESULT 15
US-08-955-471-1
Sequence 1, Application US/08955471
Patent No. 5968751
GENERAL INFORMATION:
APPLICANT: Griffin, John H.
APPLICANT: Meesters, Rolf M.
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: for Inhibiting Coagulation
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Office of Patent Counsel, The Scripps
ADDRESS: Research Institute
STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/955,471
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/295,411
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI263.0C1
TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Region
LOCATION: 1..157
OTHER INFORMATION: /note= "Protein C Light Chain"
FEATURE:
NAME/KEY: Region
LOCATION: 158..169
OTHER INFORMATION: /note= "Protein C Activation"
OTHER INFORMATION: Peptide
FEATURE:
NAME/KEY: Region
LOCATION: 170..419
OTHER INFORMATION: /note= "Protein C Heavy Chain"
US-08-955-471-1
Query Match
Best Local Similarity 81.2%; Score 160; DB 2; Length 419;
Matches 31; Conservative 2; Mismatches 11; Indels 0; Gaps 0;
Qy 1 ANSFLXLRQSLKXKICIXICDPXKXKIFEDVDTLAFWSK 44
Db 1 ANSFLBELRHSSLERECIEICDFEAKKIFQNVDDTLAFWSK 44
Search completed: March 1, 2004, 10:12:21
Job time: 17.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2004, 09:55:12 ; Search time 37.5 Seconds
(without alignments)
370.208 Million cell updates/sec

Title: SEQ1-4SUB5
Perfect score: 197
Sequence: 1 ANSFLXLRQSGSLXKXICX.....XXAKXIFEDVDLAFWSKH 44

Scoring table: ELOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP_ARCHAEL:*\n2: SP_BACTERIA:*\n3: SP_FUNGI:*\n4: SP_HUMAN:*\n5: SP_INVERTEBRATE:*\n6: SP_MAMMAL:*\n7: SP_MHC:*\n8: SP_ORNITHINE:*\n9: SP_PHAGE:*\n10: SP_PLANT:*\n11: SP RODENT:*\n12: SP_VIRUS:*\n13: SP_VIRTEBRATE:*\n14: SP_UNCLASSIFIED:*\n15: SP_VIRUS:*\n16: SP_BACTERIAP:*\n17: SP_ARCHAEL:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	151	76.6	456	6	Q9TRRO
2	140	71.1	460	11	Q91WN8
3	134	68.0	460	11	Q99PC6
4	118	59.9	55	4	Q81002
5	118	59.9	55	4	Q81002
6	118	59.9	55	4	Q81002
7	109	54.3	455	13	Q81207
8	107	54.3	455	13	Q81207
9	107	54.3	455	13	Q81207
10	105	52.5	443	13	Q804X5
11	103.5	52.5	443	13	Q804X5
12	101	51.3	440	11	Q80Y26
13	101	51.3	440	11	Q80Y26
14	101	51.3	440	11	Q80Y26
15	101	51.3	440	11	Q80Y26
16	99.5	50.5	442	13	Q804X1

17	99	50.3	679	4	Q96PQ8	Q96PQ8 homo sapien
18	97	49.2	474	13	Q80H08	Q80H08 brachydanio
19	95	48.2	469	6	Q96MD9	Q96MD9 ornithornyn
20	93	47.2	229	13	Q80J40	Q80J40 xenopus lae
21	93	47.2	434	13	Q713B6	Q713B6 brachydanio
22	92	46.7	268	4	Q8NEK6	Q8NEK6 homo sapien
23	87	44.2	425	13	Q804X7	Q804X7 gallus gall
24	87	44.2	612	13	Q804W7	Q804W7 fuqu rubrip
25	85	43.1	475	13	Q804W9	Q804W9 fuqu rubrip
26	85	43.1	497	4	Q72715	Q72715 homo sapien
27	85	43.1	650	4	Q16519	Q16519 homo sapien
28	85	43.1	650	4	Q16519	Q16519 homo sapien
29	84	42.6	100	4	Q15253	Q15253 homo sapien
30	84	42.6	622	4	Q727P3	Q727P3 homo sapien
31	82.5	41.9	542	5	Q8T613	Q8T613 halocynthia
32	81	41.1	471	13	Q804X6	Q804X6 gallus gall
33	80	40.6	446	11	Q61109	Q61109 mus musculu
34	80	40.6	461	11	Q95ND7	Q95ND7 pan troglod
35	80	40.6	461	6	Q95ND6	Q95ND6 pan troglod
36	79	40.1	441	13	Q804X2	Q804X2 fuqu rubrip
37	78	39.6	138	6	Q28994	Q28994 sus scrofa
38	78	39.6	607	13	Q91001	Q91001 gallus gall
39	78	39.6	648	6	Q29094	Q29094 sus scrofa
40	77	39.1	52	4	Q81XD5	Q81XD5 homo sapien
41	76	38.6	446	11	Q8K3U6	Q8K3U6 ractus norv
42	74	37.6	52	4	Q81XC5	Q81XC5 homo sapien
43	73.5	37.3	433	13	Q80YK1	Q80YK1 brachydanio
44	73.5	37.3	433	13	Q80YK1	Q80YK1 brachydanio
45	73	37.1	49	6	Q95ME8	Q95ME8 bos taurus

ALIGNMENTS

RESULT 1

Q9TRRO PRELIMINARY: PRT: 456 AA.
AC Q9TRRO;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Protein C precursor.
GN PROC.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Leeb T., Kopp T., Deppe A., Breen M., Matis U., Brunberg L.,
RT "Molecular characterization and chromosomal assignment of the canine
protein C gene";
RT Mamm. Genome 10:135-139(1999).
RL [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93371952; PubMed=10443005;
RA Leeb T., Pfeiffer I., Kopp T., Deppe A., Breen B.,
RT "Analysis of canine protein C gene polymorphisms";
RA Anim. Genet. 30:237-238(1999).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL: A0001979; CAA05126.1; -
DR KSSP: P04070; IAU1.
DR GO: GO:0005576; Cytoskeleton; IEA.
DR GO: GO:0005509; Cytoskeleton binding; IEA.
DR GO: GO:0004263; Fibrinogen binding; IEA.
DR GO: GO:0004233; Fibrinogen binding; IEA.
DR GO: GO:0004295; Fibrinogen binding; IEA.
DR GO: GO:0006068; Proteolysis and peptidolysis; IEA.
DR InterPro: IPR0000152; Asx_hydroxyl_S.
DR InterPro: IPR000003; Cys_ser_trypsin.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR006209; EGF_like.

DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR000294; Vtk_dep_GLA.
 DR Pfam; P00008; EGF_2.
 DR Pfam; P00594; GLA_1.
 DR Pfam; P00089; trypsin_1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; SM00101; GLABLOOD.
 DR SMART; SM00181; EGF_2.
 DR SMART; SM00069; GLA_1.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS00186; EGF_2; 2.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR EGF-like domain; Hydrolase; Protease; Serine protease; Signal.
 FT SIGNAL 1 42
 FT CHAIN 43 192 POTENTIAL, PROTEIN C LIGHT CHAIN.
 FT CHAIN 193 194 PROTEIN C CONNECTING DIPEPTIDE.
 FT CHAIN 195 456 PROTEIN C HEAVY CHAIN.
 SQ SEQUENCE 456 AA; 50813 MW; 7AD3A8C1C34E59FF CRC64;

Query Match 76.6%; Score 151; DB 6; Length 456;
 Best Local Similarity 63.6%; Pred. No. 3.8e-17;
 Matches 28; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANSFLXRRGSLRXCIXXICDPFXAKXIFEDVDITLAFMSKH 44
 DB 43 ANSFLERIRAGSLRRCMEHICDPERAKETIPNVVDITLAFMSKH 86

RESULT 2
 ID Q91WN8 PRELIMINARY; PRT; 460 AA.
 AC Q91WN8;
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Similar to protein C.
 GN PROC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Strausberg R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 DR EMBL; AC013896; AA013896.1; -
 DR HSSP; P00761; 1AUI.
 DR MGD; MGI:97771; Proc.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR000152; Asx_hydroxyl_S.
 DR InterPro; IPR009003; Cys_Ser_trypsin.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR000294; Vtk_dep_GLA.

DR Pfam; P00008; EGF_2.
 DR Pfam; P00594; GLA_1.
 DR Pfam; P00089; trypsin_1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00069; GLA_1.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR EGF-like domain; Hydrolase; Protease; Serine protease.
 SQ SEQUENCE 460 AA; 51818 MW; 011F26E6FCC274 CRC64;

Query Match 71.1%; Score 140; DB 11; Length 460;
 Best Local Similarity 59.1%; Pred. No. 2.9e-15;
 Matches 26; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 1 ANSFLXRRGSLRXCIXXICDPFXAKXIFEDVDITLAFMSKH 44
 DB 42 ANSFLERIRAGSLRRCMEHICDPERAKETIPNVVDITLAFMSKH 85

RESULT 3
 ID Q99PC6 PRELIMINARY; PRT; 460 AA.
 AC Q99PC6;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Anticoagulant protein C.
 GN PROC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/
 RA Kott I.;
 RT "Complete sequence of UC72A01."
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 DR EMBL; AF318182; AK07918.1; -
 DR HSSP; P04070; 1AUT.
 DR MGD; MGI:97771; Proc.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR000152; Asx_hydroxyl_S.
 DR InterPro; IPR009003; Cys_Ser_trypsin.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR000294; Vtk_dep_GLA.
 DR Pfam; P00008; EGF_2.
 DR Pfam; P00594; GLA_1.
 DR Pfam; P00089; trypsin_1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00069; GLA_1.
 DR SMART; SM00020; Tryp_Spc; 1.

```

DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLUT_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR EGF-like domain; Hydroxylase; Protease; Serine protease.
SQ SEQUENCE 460 AA; 51784 MW; 0235C25E9D3ED16 CRC64;

Query Match
Best Local Similarity 58.0%; Score 134; DB 11; Length 460;
Matches 25; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

Cy 1 ANSFLXLRQGSIXKXCIXXICDPFXKXIFEDVDTLAFWSKH 44
Db 42 ANSFLERKPSLERECMEICDEFEAKEIFQNVDTLAFWKY 85

RESULT 4
ID 08J002 PRELIMINARY; PRT; 55 AA.
AC 08J002;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Protein C (Fragment).
GN PROC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kinoshita S., Iida H., Inoue S., Watanabe K., Kurihara M., Wada Y.,
RA Ono M., Dongchon K., Hamasaki N.;
RT "Gene Analysis of Anticoagulation Factors in Japanese Thrombotic
RT Patients: Genetic Background of Thrombophilia in Japan.";
RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB083700; BAC21172.1;
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00069; GLA; 1.
FT NON_TER 1
FT NON_TER 55
SQ SEQUENCE 55 AA; 6527 MW; 4F89496534A78836 CRC64;

Query Match
Best Local Similarity 59.9%; Score 118; DB 4; Length 55;
Matches 24; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

Cy 1 ANSFLXLRQGSIXKXCIXXICDPFXKXIFEDVDT 37
Db 19 ANSFLERKPSLERECMEICDEFEAKEIFQNVDT 55

RESULT 5
ID 08IXB5 PRELIMINARY; PRT; 55 AA.
AC 08IXB5;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Protein C (Fragment).
GN PROC1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

```

```

CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hamasaki S., Kang D., Kinoshita S., Iida K., Inoue S., Watanabe K.,
RA Kurihara M., Wada Y., Ono M.;
RT "Gene Analysis of Anticoagulation Factors in Japanese Thrombotic
RT Patients: Genetic Background of Thrombophilia in Japan.";
RT Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB086851; BAC53631.1;
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00069; GLA; 1.
FT NON_TER 1
FT NON_TER 55
SQ SEQUENCE 55 AA; 6475 MW; 3803696534BC9289 CRC64;

Query Match
Best Local Similarity 59.9%; Score 118; DB 4; Length 55;
Matches 24; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

Cy 1 ANSFLXLRQGSIXKXCIXXICDPFXKXIFEDVDT 37
Db 19 ANSFLERKPSLERECMEICDEFEAKEIFQNVDT 55

RESULT 6
ID 063207 PRELIMINARY; PRT; 482 AA.
AC 063207;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Factor X.
GN Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Sprague-Dawley;
RX MEDLINE=86093366; PubMed=8578339;
RA Stanton C., Ross R.P., Hutson S., Wallin R.;
RT "Evidence for competition between vitamin K-dependent clotting factors
RT for intracellular processing by the vitamin K-dependent gamma-
RT carboxylase.";
RL Thromb. Res. 80:63-73(1995).
CC -11 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; X79807; CAA56202.1;
DR PIR; S49075; EXRT.
DR HSP; P00742; IXKA.
DR MEROPS; S01.216; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000152; ASX_hydroxyl_3.
DR InterPro; IPR009003; Cys_ser_trypsin.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR001438; EGF_11.
DR InterPro; IPR006209; EGF_11.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_GIA.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00594; gla; 1.

```

DR Pfam: PF00089; trypsin; 1.
 DR PRINTS; PR00022; CHYMOTRYPSIN.
 DR PRINTS; PR00010; EGFL00D.
 DR PRINTS; PR00001; GLABLOD.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; TRYP_SPC; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR EGF-like domain; Hydrolase; Protease; Serine protease.
 SQ SEQUENCE 482 AA; 54265 MW; 0284678354A698 CRC64;

Query Match 58.4%; Score 115; DB 11; Length 482;
 Best Local Similarity 43.2%; Pred. No. 6e-11;
 Matches 19; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 1 ANSFLXXLRQGSIXRCIXICDPFXAKXIFEDVDITLAFMSKH 44
 DB 41 ANSFEEIKKGNLERECVEICSFEEAREVEFEDNEKTEFWNKY 84

RESULT 7

ID Q7SY86 PRELIMINARY; PRT; 455 AA.

DT 01-OCT-2003 (TRENBLrel. 25, Created)
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipridae;
 OC Xenopodidae; Xenopus.
 NCBI_Taxid=8355;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RA MEDLINE=22341132; PubMed=12454917;
 RA Klein S.L., Strauberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 initiative";
 RT Dev. Dyn. 225:384-391 (2002).
 RL [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Whole;
 RA MEDLINE=22388257; PubMed=12477932;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buatow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Siegelman M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.J.,
 RA Rana S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Boek S.S., McGowan P.J., McKernan K.U., Malek J.A., Gunnarsson P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.W., Gay L.J., Huiyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Kravynetski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.B.,
 RA Jones S.J., Matra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [3]
 RP SEQUENCE FROM N.A.

RC TISSUE=Whole;
 RA Klein S., Strauberg R.;
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC054968; AAH54968.1; --
 KW Hypothetical protein.
 SQ SEQUENCE 455 AA; 51811 MW; 07C027EDB495330 CRC64;

Query Match 55.3%; Score 109; DB 13; Length 455;
 Best Local Similarity 50.0%; Pred. No. 6e-10;
 Matches 22; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANSFLXXLRQGSIXRCIXICDPFXAKXIFEDVDITLAFMSKH 44
 DB 49 ANFMELKPKGSILRECEKCDFEAREIFETEDITLFWNKY 92

RESULT 8

ID Q8N2N6 PRELIMINARY; PRT; 231 AA.

DT 01-OCT-2002 (TRENBLrel. 22, Created)
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Hypothetical protein FLJ50093.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_Taxid=9606;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Itoigai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
 RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hiro Y., Saito K.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,
 RA Maehara Y., Ono T., Okano K., Yoshikawa Y., Aotaka S., Sasaki N.,
 RA Hattori A., Okumura K., Iwayanagi T., Minomiya K.;
 RT "NEDO human cDNA sequencing project";
 RT Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AK074574; BAC1069.1; --
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR00294; VitK_dep_GLA.
 DR Pfam; PF00594; GLA; 1.
 DR PRINTS; PR00001; GLABLOD.
 DR SMART; SM00069; GLA; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 231 AA; 25844 MW; 8A373B0D5C1D0D81 CRC64;

Query Match 54.3%; Score 107; DB 4; Length 231;
 Best Local Similarity 43.2%; Pred. No. 6.3e-10;
 Matches 18; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

QY 1 ANSFLXXLRQGSIXRCIXICDPFXAKXIFEDVDITLAFW 41
 DB 20 ANFELRLRQGLTERECMEICSYERKVEFENKKEKTFW 60

RESULT 9

ID Q804X5 PRELIMINARY; PRT; 433 AA.

DT 01-JUN-2003 (TRENBLrel. 24, Created)
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Anticoagulant protein C precursor (EC 3.4.21.69).
 NCBI_Taxid=9606;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RA Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinoptera; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

```

OC Gallus.
RX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Davidson C.J., Hirt R.P., Lal K., Snell P., Elgar G.,
RT "Comparative genome analysis and molecular evolution of blood
RT coagulation genes from Gallus gallus and Fugu rubripes."
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF465270; AAO3365.1; -.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0005509; F:calcium ion binding; IEA.
DR GO: GO:0004263; F:chymotrypsin activity; IEA.
DR GO: GO:0016787; F:hydrolyase activity; IEA.
DR GO: GO:0003808; F:protein C (activated) activity; IEA.
DR GO: GO:0004285; F:trypsin activity; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR000152; Asx hydroxyl S.
DR InterPro: IPR009003; Cys Ser trypsin.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR006209; EGF_Like.
DR InterPro: IPR002383; GLA blood.
DR InterPro: IPR006210; IEGF.
DR InterPro: IPR001254; peptidase S1.
DR InterPro: IPR001314; peptidase S1A.
DR InterPro: IPR000294; Vitr_dep_GLA.
DR Pfam: PF00008; EGF_1.
DR Pfam: PF00594; GLA_1.
DR Pfam: PF00089; trypsin_1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00181; EGF_2.
DR SMART: SM00179; EGF_Ca_1.
DR SMART: SM00069; GLA_1.
DR SMART: SM00020; Tryp_SPC_1.
DR PROSITE: PS00010; ASX_HYDROXYL_1.
DR PROSITE: PS00022; EGF_1.
DR PROSITE: PS01186; EGF_2_2.
DR PROSITE: PS01187; EGF_Ca_1.
DR PROSITE: PS00011; GLU_CARBOXYLATION_1.
DR PROSITE: PS00240; TRYPSIN_DOM_1.
DR PROSITE: PS00134; TRYPSIN_HIS_1.
DR PROSITE: PS00135; TRYPSIN_SER_1.
DR HydroLase: 433 AA; 46689 MW; E09DDE56D7DA23 CRC64;
SQ
Query Match 54.3%; Score 107; DB 13; Length 433;
Best Local Similarity 50.0%; Pred. No. 1, 2e-09;
Matches 22; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

```

```

OY 1 ANSFLXLRQGSIXKXCIXXICDPFXAKXIFEDVDPTLAFMSKH 44
DB 40 ANSFLXLRQGSIXKXCIXXICDPFXAKXIFEDVDPTLAFMSKH 83

```

```

RESULT 10
Q7SKH8 PRELIMINARY; PRT; 524 AA.
AC Q7SKH8;
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Hypothetical protein.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Body;
RX MEDLINE=22386257; PubMed=12477932;

```

```

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore I., Wax S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uebachs T.B., Toshitsugu S., Carninci P., Prange C.,
RA Bha S.S., Loggellano N.A., Peters G.J., Adamson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Rochard S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Mazy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Kelley J., Helton E., Kertman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman U.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
RA Krzywicki M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC Tissue=Body;
RA Strausberg R.L.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC055596; AAH55596.1; -.
KW Hypothetical protein.
SQ
Query Match 53.3%; Score 105; DB 13; Length 524;
Best Local Similarity 43.2%; Pred. No. 3, 4e-09;
Matches 19; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

```

```

OY 1 ANSFLXLRQGSIXKXCIXXICDPFXAKXIFEDVDPTLAFMSKH 44
DB 42 ANSFLXLRQGSIXKXCIXXICDPFXAKXIFEDVDPTLAFMSKH 85

```

```

RESULT 11
Q8H9C9 PRELIMINARY; PRT; 443 AA.
AC Q8H9C9;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Coagulation factor VIII.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Hannamhaiah R., Day K., Jagadeeswaran P.;
RT "Comprehensive analysis of blood coagulation pathways in Zebrafish:
RT Evolution of coagulation factor genes and identification of zebrafish
RT factor VIII."
RL Blood Cells Mol. Dis. 0:0-0(2002).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL: AF519546; AAM88342.1; -.
DR EMBL: AF519546; AAM71000.1; -.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0005509; F:calcium ion binding; IEA.
DR GO: GO:0004263; F:chymotrypsin activity; IEA.
DR GO: GO:0006233; F:peptidase activity; IEA.
DR GO: GO:0004295; F:trypsin activity; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR009003; Cys Ser trypsin.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR006209; EGF_Like.
DR InterPro: IPR002383; GLA blood.
DR InterPro: IPR006210; IEGF.

```

DR InterPro: IPR001254; Peptidase_S1.
DR InterPro: IPR001314; Peptidase_S1A.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF_1.
DR Pfam: PF00594; Gla; 1.
DR PRINTS: PR00089; trypsin.1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00181; EGF_2.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; Tryp_Spec; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR EGF-like domain; Hydrolase; Protease; Serine protease.
KW SEQUENCE 443 AA; 48823 MW; 2D2504718AE94FF4 CRC64;
SQ

Query Match 52.5%; Score 103.5; DB 13; Length 443;
Best Local Similarity 47.6%; Pred. No. 5.1e-09;
Matches 20; Conservative 7; Mismatches 14; Indels 1; Gaps 1;
DB 38 ANSGFLBEMKAGNLERCEVERICDYEAREVFEEDDDRTKQFW 79
QY 1 ANS-FLXXLRQGSLSKXCIXXICDPFXAXXIFEDVDTLAFW 41
ID 080126 PRELIMINARY; PRT; 340 AA.
AC 080126;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE F10 protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=22386257; PubMed=12477932;
RA Strausberg R.J., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stadelson M., Soares M.B., Bonaldo M.F., Cassavatt T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Pangue C.,
RA Raha S.S., Loughran N.A., Peters G.J., Abramson R.D., Millen S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultix S.W.,
RA Villalón D.K., Wuzny K.D., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy U., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Alakeshri R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.J., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RA Strausberg R.J.,
RT Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC050219; AAH50219.1;
DR GO: GO:0005576; Cytoplasmic; IEA.
DR GO: GO:0005509; F:calcium ion binding; IEA.

DR GO: GO:0004295; F:trypsin activity; IEA.
DR GO: GO:0005508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR00152; Asx_Hydroxyl_S.
DR InterPro: IPR009003; Cys_ser_crypsin.
DR InterPro: IPR00742; EGF_2.
DR InterPro: IPR01681; EGF_CA.
DR InterPro: IPR01438; EGF_II.
DR InterPro: IPR006209; EGF-like.
DR InterPro: IPR00283; GLA_blood.
DR InterPro: IPR006210; IEGF.
DR InterPro: IPR001254; Peptidase_S1.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF_1.
DR Pfam: PF00594; Gla; 1.
DR PRINTS: PR00010; EGFLOOD.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00181; EGF_2.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00069; GLA; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
SQ SEQUENCE 340 AA; 38359 MW; EE252D6157720811 CRC64;
Query Match 51.3%; Score 101; DB 11; Length 340;
Best Local Similarity 38.6%; Pred. No. 1e-08;
Matches 17; Conservative 10; Mismatches 17; Indels 0; Gaps 0;
DB 53 ANSFLBEMKAGNLERCEVERICDYEAREVFEEDDDRTKQFW 96
QY 1 ANS-FLXXLRQGSLSKXCIXXICDPFXAXXIFEDVDTLAFW 41
ID 054740 PRELIMINARY; PRT; 481 AA.
AC 054740;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Coagulation factor X precursor (SC 3.4.21.6).
GN F10 OR Fx10.
OS Mus musculus (Mouse).
OC Placental placentarct.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=9845493; PubMed=9793672;
RA Heidemann H.R., Konermann R.E.,
RT "Cloning and recombinant expression of mouse coagulation factor X."
RL Thromb. Res. 92:33-41(1998).
CC -1. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL: AJ222677; CAAL0933.1;
DR HSSP: P00742; 1XKA.
DR MEROPS: S01_216; -.
DR MCD: MCD:103107; F10.
DR GO: GO:0005576; Cytoplasmic; IEA.
DR GO: GO:0046821; C:extrachromosomal DNA; IEA.
DR GO: GO:0003804; F:bioid coagulation factor X activity; IEA.
DR GO: GO:0005509; F:calcium ion binding; IEA.
DR GO: GO:0004295; F:chymotrypsin activity; IEA.
DR GO: GO:0008263; F:peptidase activity; IEA.
DR GO: GO:0004295; F:trypsin activity; IEA.
DR GO: GO:0005508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR000152; Asx_Hydroxyl_S.
DR InterPro: IPR009003; Cys_ser_crypsin.

```
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001861; EGF_Ca.
DR InterPro: IPR001438; EGF_11.
DR InterPro: IPR006209; EGF_1ike.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Peptidase_S1.
DR InterPro: IPR001354; Peptidase_S1A.
DR InterPro: IPR000294; Vltk_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00594; Gla; 1.
DR Pfam: PF00083; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00010; EGFLOOD.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; TRYP_SPC; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS00240; TRYPsin_DOM; 1.
DR PROSITE: PS00134; TRYPsin_HIS; 1.
DR PROSITE: PS00135; TRYPsin_SER; 1.
DR EGF-like domain; Hydrolase; Protease; Serine protease; Signal;
KW plasmaid.
FT SIGNAL 1 40 POTENTIAL
FT CHAIN 41 481 COAGULATION FACTOR X.
SQ SEQUENCE 481 AA; 53986 MW; CF702DESEPD97AE CRC64;

Query Match 51.3%; Score 101; DB 11; Length 481;
Best Local Similarity 38.6%; Pred. No. 1.5e-08;
Matches 17; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

CY 1 ANSFLXLRQGSIXKXICDPFXKXKIFEDVDTLAFWSKH 44
DB 41 ANSFPEFKGNLEKHECMETICSYEVRNRFEDDEKTKRWTKY 84

RESULT 14
ID Q99L32 PRELIMINARY; PRT; 481 AA.
AC Q99L32;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Coagulation factor X.
GN F10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RT Submitted (Feb-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL: EC003877; AA03877.1; -.
DR HSSP: P00742; 1XKA.
DR MEROPS: S01.216; -.
DR MGD: MGI:103107; F10.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0005509; F:calcium ion binding; IEA.
DR GO: GO:0004263; F:chymotrypsin activity; IEA.
DR GO: GO:0008233; F:peptidase activity; IEA.
DR GO: GO:0004295; F:trypsin activity; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR000152; Asx_HydroxyL_S
DR InterPro: IPR003803; Cys_Ser_Trypsin.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001861; EGF_Ca.
DR InterPro: IPR001438; EGF_11.
DR InterPro: IPR001354; EGF_1like.
```

```
DR InterPro: IPR006209; EGF_1like.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Peptidase_S1.
DR InterPro: IPR001314; Peptidase_S1A.
DR InterPro: IPR000294; Vltk_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00594; Gla; 1.
DR Pfam: PF00083; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00010; EGFLOOD.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; TRYP_SPC; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS00240; TRYPsin_DOM; 1.
DR PROSITE: PS00134; TRYPsin_HIS; 1.
DR PROSITE: PS00135; TRYPsin_SER; 1.
DR EGF-like domain; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 481 AA; 54004 MW; BD88E96C8A0B7E7F CRC64;

Query Match 51.3%; Score 101; DB 11; Length 481;
Best Local Similarity 38.6%; Pred. No. 1.5e-08;
Matches 17; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

CY 1 ANSFLXLRQGSIXKXICDPFXKXKIFEDVDTLAFWSKH 44
DB 41 ANSFPEFKGNLEKHECMETICSYEVRNRFEDDEKTKRWTKY 84

RESULT 15
ID O88947 PRELIMINARY; PRT; 481 AA.
AC O88947;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Coagulation factor X precursor.
GN F10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-C57BL/6 J. CBA. TISSUE: Liver;
RX MEDLINE: 96347933; PubMed: 9687791;
RA Liang Z., Cooper A., Deford M.E., Carmeliet P., Collen D.,
RA Castellino F.J., Rosen E.D.;
RT "Cloning and characterization of a cDNA encoding murine coagulation
RT factor X."
RL Thromb. Haemost. 80:87-91(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=129Sj;
RA Cooper A., Liang Z., Castellino F.J., Rosen E.D.;
RT "Cloning and characterization of the murine Factor X Gene."
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL: AF087644; AAC6345.1; -.
DR EMBL: AF211347; AAF22960.1; -.
DR HSSP: P00742; 1XKA.
DR MEROPS: S01.216; -.
DR MGD: MGI:103107; F10.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0005509; F:calcium ion binding; IEA.
DR GO: GO:0004263; F:chymotrypsin activity; IEA.
DR GO: GO:0008233; F:peptidase activity; IEA.
DR GO: GO:0004295; F:trypsin activity; IEA.
```


DR GO;0006508; F:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR000152; Asx_hydroxyl_S.
 DR InterPro; IPR009003; Cys_Ser_Trypsin.
 DR InterPro; IPR00742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR001438; EGF_II.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR00294; Vltk_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00594; GLA; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00010; EGFBLOOD.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00178; EGF_CA; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLUT_CARBOXYLATION; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR EGF-like domain; Hydrolase; Protease; Serine protease; Signal.
 FT SIGNAL 1 40
 FT CHAIN 1 481
 SQ SEQUENCE 481 AA; 54018 MW; 8AC09DESEF9D271E CRC64;

Query Match 51.3%; Score 101; DB 11; Length 481;
 Best Local Similarity 38.6%; Pred. No. 1.5e-08;
 Matches 17; Conservative 10; Mismatches 17; Indels 0; Gaps 0;
 Qy 1 ANSPFLXUNQSLXRXICIXIXICDFFXAXKIFEDVDITLAFWSKH 44
 Db 41 ANSPFEPFKGNLFRRCMEICSYEVREIFEDDEKTKETWTKY 84

Search completed: March 1, 2004, 10:02:52
 Job time : 38.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2004, 10:01:28 ; Search time 28 Seconds
(without alignments)
331.812 Million cell updates/sec

Title: SEQ1-4SUBS

Sequence: 1 ANSFLXLRGSLRXKXIX.....XXAKXIFEDVDTLAFWSKH 44

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 809742 seqs, 21153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

Published Applications_AA:
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCF_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCFUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	179	90.9	419	US-10-182-263-6	Sequence 6, Appli
2	179	90.9	419	US-10-168-407-5	Sequence 6, Appli
3	179	90.9	419	US-10-168-407-6	Sequence 6, Appli
4	174	88.3	419	US-10-182-263-2	Sequence 3, Appli
5	174	88.3	419	US-10-182-263-4	Sequence 3, Appli
6	174	88.3	419	US-10-182-263-5	Sequence 3, Appli
7	174	88.3	419	US-10-168-407-3	Sequence 3, Appli
8	174	88.3	419	US-10-168-407-4	Sequence 3, Appli
9	160	81.2	44	US-10-298-330-1	Sequence 4, Appli
10	160	81.2	419	US-09-978-917A-4	Sequence 4, Appli
11	160	81.2	419	US-10-182-263-1	Sequence 1, Appli
12	160	81.2	419	US-10-168-407-1	Sequence 1, Appli
13	160	81.2	461	US-08-978-917A-2	Sequence 2, Appli
14	160	81.2	461	US-10-182-263-2	Sequence 2, Appli
15	160	81.2	461	US-10-168-407-2	Sequence 2, Appli

16	116	58.9	44	US-10-298-330-2	Sequence 2, Appli
17	110	55.8	138	US-10-360-101-232	Sequence 23, App
18	110	55.8	488	US-10-348-504-44	Sequence 44, Appl
19	110	55.8	488	US-10-407-123-27	Sequence 27, Appl
20	106	53.8	44	US-10-298-330-18	Sequence 18, Appl
21	99	50.3	42	US-10-038-854-97	Sequence 97, Appl
22	99	50.3	406	US-09-782-587B-3	Sequence 3, Appli
23	99	50.3	406	US-10-383-898-1	Sequence 1, Appli
24	99	50.3	406	US-10-383-898-1	Sequence 1, Appli
25	99	50.3	466	US-10-017-121-2	Sequence 2, Appli
26	96	48.7	44	US-10-298-330-3	Sequence 3, Appli
27	96	48.7	406	US-09-782-587B-1	Sequence 1, Appli
28	96	48.7	406	US-10-109-498-1	Sequence 1, Appli
29	96	48.7	406	US-10-255-032-1	Sequence 1, Appli
30	96	48.7	406	US-10-281-727-1	Sequence 1, Appli
31	96	48.7	406	US-10-386-898-7	Sequence 7, Appli
32	95	48.2	405	US-10-360-101-235	Sequence 225, Appl
33	91	46.2	40	US-10-298-330-23	Sequence 23, Appli
34	90	45.7	44	US-10-298-330-4	Sequence 23, Appli
35	89	45.2	40	US-10-298-330-25	Sequence 23, Appli
36	85	43.1	40	US-10-298-330-22	Sequence 22, Appli
37	84.5	42.9	96	US-09-759-130B-313	Sequence 313, App
38	84.5	42.9	96	US-10-189-123-43	Sequence 43, Appl
39	84.5	42.9	96	US-10-188-495-43	Sequence 43, Appl
40	84.5	42.9	209	US-09-759-130B-312	Sequence 312, App
41	84.5	42.9	209	US-10-189-123-42	Sequence 42, Appl
42	84.5	42.9	209	US-10-188-495-42	Sequence 42, Appl
43	84.5	42.9	226	US-09-759-130B-310	Sequence 310, App
44	84.5	42.9	226	US-10-189-123-40	Sequence 40, Appl
45	84.5	42.9	226	US-10-188-495-40	Sequence 40, Appl

ALIGNMENTS

RESULT 1
US-10-182-263-6
Sequence 6, Application US/10182263
Publication No. US20030022354A1
GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
APPLICANT: Jones, Bryan E
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRENT FILING DATE: 2002-07-22
PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 419
TYPE: PRT
ORGANISM: Homo sapiens
US-10-182-263-6

Query Match 90.9%; Score 179; DB 14; Length 419;
Best Local Similarity 79.5%; Pred. No. 3, 9e-22;
Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ANSFLXLRGSLRXKXIXICPFXAKXIFEDVDTLAFWSKH 44
DB 1 ANSFLXLRGSLRXKXIXICPFXAKXIFEDVDTLAFWSKH 44

RESULT 2
US-10-168-407-5
Sequence 5, Application US/10168407
Publication No. US20030207435A1
GENERAL INFORMATION:

APPLICANT: Geriltz, Bruce E
APPLICANT: Jones, Bryan E
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13610
CURRENT APPLICATION NUMBER: US/10/168,407
CURRENT FILING DATE: 2002-11-04
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 419
TYPE: PRT
ORGANISM: Homo sapiens
US-10-168-407-5

Query Match 90.9%; Score 179; DB 15; Length 419;
Best Local Similarity 79.5%; Pred. No. 3.9e-22;
Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ANSFLXLRQGSILKRCIXXICDPFXAKXIFEDVDTLAFWSKH 44
DB 1 ANSFLBELRQGSLERECEIEICDPFEAKXIFEDVDTLAFWSKH 44

RESULT 3
US-10-168-407-6
Sequence 6, Application US/10168407
Publication No. US20030207435A1
GENERAL INFORMATION:
APPLICANT: Geriltz, Bruce E
APPLICANT: Jones, Bryan E
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13610
CURRENT APPLICATION NUMBER: US/10/168,407
CURRENT FILING DATE: 2002-11-04
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 419
TYPE: PRT
ORGANISM: Homo sapiens
US-10-168-407-6

Query Match 90.9%; Score 179; DB 15; Length 419;
Best Local Similarity 79.5%; Pred. No. 3.9e-22;
Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ANSFLXLRQGSILKRCIXXICDPFXAKXIFEDVDTLAFWSKH 44
DB 1 ANSFLBELRQGSLERECEIEICDPFEAKXIFEDVDTLAFWSKH 44

RESULT 4
US-10-182-263-3
Sequence 3, Application US/10182263
Publication No. US20030022354A1
GENERAL INFORMATION:
APPLICANT: Geriltz, Bruce E
APPLICANT: Jones, Bryan E
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: 60/189199
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 419
TYPE: PRT
ORGANISM: Homo sapiens

US-10-182-263-3

Query Match 88.3%; Score 174; DB 14; Length 419;
Best Local Similarity 77.3%; Pred. No. 2.8e-21;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANSFLXLRQGSILKRCIXXICDPFXAKXIFEDVDTLAFWSKH 44
DB 1 ANSFLBELRQGSLERECEIEICDPFEAKXIFEDVDTLAFWSKH 44

RESULT 5
US-10-182-263-4
Sequence 4, Application US/10182263
Publication No. US20030022354A1
GENERAL INFORMATION:
APPLICANT: Geriltz, Bruce E
APPLICANT: Jones, Bryan E
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: 60/189199
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 419
TYPE: PRT
ORGANISM: Homo sapiens
US-10-182-263-4

Query Match 88.3%; Score 174; DB 14; Length 419;
Best Local Similarity 77.3%; Pred. No. 2.8e-21;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANSFLXLRQGSILKRCIXXICDPFXAKXIFEDVDTLAFWSKH 44
DB 1 ANSFLBELRQGSLERECEIEICDPFEAKXIFEDVDTLAFWSKH 44

RESULT 6
US-10-182-263-5
Sequence 5, Application US/10182263
Publication No. US20030022354A1
GENERAL INFORMATION:
APPLICANT: Geriltz, Bruce E
APPLICANT: Jones, Bryan E
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: 60/189199
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 419
TYPE: PRT
ORGANISM: Homo sapiens
US-10-182-263-5

Query Match 88.3%; Score 174; DB 14; Length 419;
Best Local Similarity 77.3%; Pred. No. 2.8e-21;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANSFLXLRQGSILKRCIXXICDPFXAKXIFEDVDTLAFWSKH 44

DB 1 ANSFLELRHSGSLRRCIEICDFEAKEIFEDVDITLAFWSKH 44

RESULT 7

US-10-168-407-3

Sequence 3, Application US/10168407

Publication No. US20030207435A1

GENERAL INFORMATION:

APPLICANT: Gerlitz, Bruce E

APPLICANT: Jones, Bryan E

TITLE OF INVENTION: PROTEIN C DERIVATIVES

FILE REFERENCE: X-13610

CURRENT APPLICATION NUMBER: US/10/168,407

CURRENT FILING DATE: 2002-11-04

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn version 3.1

SEQ ID NO 3

LENGTH: 419

TYPE: PRT

ORGANISM: Homo sapiens

US-10-168-407-3

Query Match

Best Local Similarity 88.3%; Score 174; DB 15; Length 419;

Best Local Similarity 77.3%; Pred. No. 2, 8e-21;

Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANSFLLXLRQGSILRXKICIXXICDFEYXAKXIFEDVDITLAFWSKH 44

DB 1 ANSFLELRHSGSLRRCIEICDFEAKEIFEDVDITLAFWSKH 44

RESULT 8

US-10-168-407-4

Sequence 4, Application US/10168407

Publication No. US20030207435A1

GENERAL INFORMATION:

APPLICANT: Gerlitz, Bruce E

APPLICANT: Jones, Bryan E

TITLE OF INVENTION: PROTEIN C DERIVATIVES

FILE REFERENCE: X-13610

CURRENT APPLICATION NUMBER: US/10/168,407

CURRENT FILING DATE: 2002-11-04

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn version 3.1

SEQ ID NO 4

LENGTH: 419

TYPE: PRT

ORGANISM: Homo sapiens

US-10-168-407-4

Query Match

Best Local Similarity 88.3%; Score 174; DB 15; Length 419;

Best Local Similarity 77.3%; Pred. No. 2, 8e-21;

Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANSFLLXLRQGSILRXKICIXXICDFEYXAKXIFEDVDITLAFWSKH 44

DB 1 ANSFLELRHSGSLRRCIEICDFEAKEIFEDVDITLAFWSKH 44

RESULT 9

US-10-298-330-1

Sequence 1, Application US/10298330

Publication No. US20030100506A1

GENERAL INFORMATION:

APPLICANT: Nelesstuen, Gary L.

TITLE OF INVENTION: Modified Vitamin K-Dependent

TITLE OF INVENTION: Polypeptides

FILE REFERENCE: 08531-127001

CURRENT APPLICATION NUMBER: US/10/298,330

CURRENT FILING DATE: 2002-11-18

PRIOR APPLICATION NUMBER: 09/497,591

PRIOR FILING DATE: 2000-02-03

PRIOR APPLICATION NUMBER: 09/302,239

PRIOR FILING DATE: 1998-04-29

PRIOR APPLICATION NUMBER: 08/955,636

PRIOR FILING DATE: 1997-10-23

NUMBER OF SEQ ID NOS: 27

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1

LENGTH: 44

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: VARIANT

LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29

OTHER INFORMATION: Xaa = gamma carboxylutamic or glutamic acid

US-10-298-330-1

Query Match

Best Local Similarity 81.2%; Score 160; DB 14; Length 44;

Best Local Similarity 90.9%; Pred. No. 5, 7e-20;

Matches 40; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ANSFLLXLRQGSILRXKICIXXICDFEYXAKXIFEDVDITLAFWSKH 44

DB 1 ANSFLLXLRHSGSLRRCIEICDFEYXAKXIFEDVDITLAFWSKH 44

RESULT 10

US-09-978-917A-4

Sequence 4, Application US/09978917A

Publication No. US20030027299A1

GENERAL INFORMATION:

APPLICANT: Maxygen Aps; Maxygen Holdings

TITLE OF INVENTION: Protein C or activated protein C-like molecules

FILE REFERENCE: 0219us310 - protein C

CURRENT APPLICATION NUMBER: US/09/978,917A

CURRENT FILING DATE: 2001-10-17

NUMBER OF SEQ ID NOS: 48

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 4

LENGTH: 419

TYPE: PRT

ORGANISM: Homo sapiens

US-09-978-917A-4

Query Match

Best Local Similarity 81.2%; Score 160; DB 10; Length 419;

Best Local Similarity 70.5%; Pred. No. 7e-19;

Matches 31; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 1 ANSFLLXLRQGSILRXKICIXXICDFEYXAKXIFEDVDITLAFWSKH 44

DB 1 ANSFLELRHSGSLRRCIEICDFEAKEIFEDVDITLAFWSKH 44

RESULT 11

US-10-182-263-1

Sequence 1, Application US/10182263

Publication No. US20030022354A1

GENERAL INFORMATION:

APPLICANT: Gerlitz, Bruce E

APPLICANT: Jones, Bryan E

TITLE OF INVENTION: PROTEIN C DERIVATIVES

FILE REFERENCE: X-13611

CURRENT APPLICATION NUMBER: US/10/182,263

CURRENT FILING DATE: 2002-07-22

PRIOR APPLICATION NUMBER: 60/181948

PRIOR FILING DATE: 2002-02-11

PRIOR APPLICATION NUMBER: 60/189199

PRIOR FILING DATE: 2000-03-14

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn version 3.1

SEQ ID NO 1

LENGTH: 419

TYPE: PRT

ORGANISM: Homo sapiens
US-10-182-263-1

Query Match 81.2%; Score 160; DB 14; Length 419;
Best Local Similarity 70.5%; Pred. No. 7e-19;
Matches 31; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 1 ANSFLXXLRGSLRXICIXXICDPXXAKXIFEDVDDTLAFWSKH 44
DB 1 ANSFLBELRHSSLSRECEIEICDFEAKEIFQVNDTLAFWSKH 44

RESULT 12:
US-10-168-407-1
Sequence 1, Application US/10168407
Publication No. US20030207435A1
GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
APPLICANT: Jones, Bryan E
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13610
CURRENT APPLICATION NUMBER: US/10/168,407
CURRENT FILING DATE: 2002-11-04
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 419
TYPE: PRT
ORGANISM: Homo sapiens
US-10-168-407-1

Query Match 81.2%; Score 160; DB 15; Length 419;
Best Local Similarity 70.5%; Pred. No. 7e-19;
Matches 31; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 1 ANSFLXXLRGSLRXICIXXICDPXXAKXIFEDVDDTLAFWSKH 44
DB 1 ANSFLBELRHSSLSRECEIEICDFEAKEIFQVNDTLAFWSKH 44

RESULT 13
US-09-978-917A-2
Sequence 2, Application US/09978917A
Publication No. US2003027299A1
GENERAL INFORMATION:
APPLICANT: Maxygen Aps; Maxygen Holdings
TITLE OF INVENTION: Protein C or activated protein C-like molecules
FILE REFERENCE: 0219us310 - protein C
CURRENT APPLICATION NUMBER: US/09/978,917A
CURRENT FILING DATE: 2001-10-17
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 461
TYPE: PRT
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: SIGNAL
LOCATION: (1)...(42)
FEATURE:
NAME/KEY: CHAIN
LOCATION: (43)...(461)
US-09-978-917A-2

Query Match 81.2%; Score 160; DB 10; Length 461;
Best Local Similarity 70.5%; Pred. No. 7.8e-19;
Matches 31; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 1 ANSFLXXLRGSLRXICIXXICDPXXAKXIFEDVDDTLAFWSKH 44
DB 43 ANSFLBELRHSSLSRECEIEICDFEAKEIFQVNDTLAFWSKH 86

RESULT 14
US-10-182-263-2
Sequence 2, Application US/10182263
Publication No. US2003022354A1
GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
APPLICANT: Jones, Bryan E
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: 60/189199
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 461
TYPE: PRT
ORGANISM: Homo sapiens
US-10-182-263-2

Query Match 81.2%; Score 160; DB 14; Length 461;
Best Local Similarity 70.5%; Pred. No. 7.8e-19;
Matches 31; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 1 ANSFLXXLRGSLRXICIXXICDPXXAKXIFEDVDDTLAFWSKH 44
DB 43 ANSFLBELRHSSLSRECEIEICDFEAKEIFQVNDTLAFWSKH 86

RESULT 15
US-10-168-407-2
Sequence 2, Application US/10168407
Publication No. US20030207435A1
GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
APPLICANT: Jones, Bryan E
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13610
CURRENT APPLICATION NUMBER: US/10/168,407
CURRENT FILING DATE: 2002-11-04
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 461
TYPE: PRT
ORGANISM: Homo sapiens
US-10-168-407-2

Query Match 81.2%; Score 160; DB 15; Length 461;
Best Local Similarity 70.5%; Pred. No. 7.8e-19;
Matches 31; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 1 ANSFLXXLRGSLRXICIXXICDPXXAKXIFEDVDDTLAFWSKH 44
DB 43 ANSFLBELRHSSLSRECEIEICDFEAKEIFQVNDTLAFWSKH 86

Search completed: March 1, 2004, 10:11:10
Job time : 28 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

CM protein - protein search, using sw model

Run on: March 1, 2004, 09:54:37 ; Search time 50 Seconds

(without alignments)
248.642 Million cell updates/sec

Title: SEQ1-32GLU-33ASP

Perfect score: 198
Sequence: 1 ANSFLXLRHSLXRCIX.....XXAKXIFEDVDTAFMSKH 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_29Jan04.*

1: geneseqp19808.*
2: geneseqp19908.*
3: geneseqp20008.*
4: geneseqp20018.*
5: geneseqp20028.*
6: geneseqp20038.*
7: geneseqp20048.*
8: geneseqp20058.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	180	90.9	44	AAV18297	AAV18297 Modified
2	176	88.9	419	AAAB82676	AAAB82676 Human pro
3	176	88.9	419	AAAB82675	AAAB82675 Human pro
4	176	88.9	419	AAAB82678	AAAB82678 Human pro
5	176	88.9	419	AAAB82677	AAAB82677 Human pro
6	176	88.9	419	AAAB82679	AAAB82679 Human pro
7	174	87.9	45	AAAB79947	AAAB79947 Human pro
8	172	86.9	44	AAV18299	AAV18299 Modified
9	172	86.9	44	AAV18309	AAV18309 Modified
10	172	86.9	44	AAV18309	AAV18309 Modified
11	172	86.9	44	AAV18303	AAV18303 Human pro
12	172	86.9	44	AAAB36402	AAAB36402 Human pro
13	172	86.9	44	AAAB50094	AAAB50094 Human vit
14	172	86.9	45	AAW75710	AAW75710 Partial h
15	172	86.9	45	AAAB79947	AAAB79947 Human pro
16	172	86.9	45	AAAB71155	AAAB71155 Human pro
17	172	86.9	45	AAV56803	AAV56803 Truncated
18	172	86.9	419	AAAB35760	AAAB35760 Protein C
19	172	86.9	419	AAAB2753	AAAB2753 Primary s
20	172	86.9	419	AAAB82673	AAAB82673 Wild-type
21	172	86.9	419	AAAB36896	AAAB36896 Human pro
22	172	86.9	419	AAAB36897	AAAB36897 Human pro
23	172	86.9	419	AAAB36898	AAAB36898 Human pro
24	172	86.9	419	AAAB36894	AAAB36894 Human pro
25	172	86.9	419	AAAB08625	AAAB08625 Human mat

26	172	86.9	419	AAU99005	AAU99005 Human pro
27	172	86.9	419	AAU99006	AAU99006 Human pro
28	172	86.9	419	AAU99008	AAU99008 Human pro
29	172	86.9	419	AAU99018	AAU99018 Human pro
30	172	86.9	419	AAU99026	AAU99026 Human pro
31	172	86.9	419	AAU99037	AAU99037 Human pro
32	172	86.9	419	AAU99049	AAU99049 Human pro
33	172	86.9	419	AAU99063	AAU99063 Human pro
34	172	86.9	419	AAU99072	AAU99072 Human pro
35	172	86.9	419	AAU99083	AAU99083 Human pro
36	172	86.9	419	AAU99084	AAU99084 Human pro
37	172	86.9	419	AAU99012	AAU99012 Human pro
38	172	86.9	419	AAU99021	AAU99021 Human pro
39	172	86.9	419	AAU99033	AAU99033 Human pro
40	172	86.9	419	AAU99039	AAU99039 Human pro
41	172	86.9	419	AAU99047	AAU99047 Human pro
42	172	86.9	419	AAU99050	AAU99050 Human pro
43	172	86.9	419	AAU99076	AAU99076 Human pro
44	172	86.9	419	AAU99088	AAU99088 Human pro
45	172	86.9	419	AAU99097	AAU99097 Human pro

ALIGNMENTS

RESULT 1	
AAV18297	
ID AAV18297 standard; peptide; 44 AA.	
AC AAV18297;	
DT 17-AUG-1999 (first entry)	
DE Modified GUA domain of vitamin K-dependent protein.	
DE GUA domain; muten; vitamin K-dependent protein; clotting disorder;	
KW therapy.	
OS Homo sapiens.	
OS Synthetic.	
FT Key	Location/Qualifiers
FT Msc-difference 1..44	/note= "Xaa= gamma-carboxyglutamic acid, or glutamic acid"
FT	
FN WO920767-A1.	
PD 23-APR-1999.	
PF 20-OCT-1996; 98WO-US022152.	
PR 23-OCT-1997; 97US-00955636.	
PI (MINT) UNIV MINNESOTA.	
PI Nelsetuen GL;	
DR WPI; 1999-288309/24.	
PT Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid	
PT domain, useful for treating clotting disorders.	
PS Claim 6, Page 78; 86pp; English.	
XX This sequence represents a modified GUA (gamma-carboxyglutamic acid)	
XX domain. The invention relates to a vitamin K-dependent polypeptide	
XX comprising a modified GUA domain containing an amino acid substitution	
XX which enhances membrane binding of the modified polypeptide as compared	
XX to the native polypeptide. The polypeptide is used to treat a clotting	
XX disorder by decreasing or increasing clot formation. Modification of the	
XX GUA domain results in a protein which has enhanced membrane binding	
XX affinity as compared to the native protein	

Query Match	Best Local Similarity	Score 160;	DB 2;	Length 44;
Matches 44;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
<p>QY 1 ANSFLXXLRHSSILXRCIXICDFFXXAXIFEDVDTLAFWSKH 44 1 ANSFLXXLRHSSILXRCIXICDFFXXAXIFEDVDTLAFWSKH 44</p>				
<p>Db</p>				
<p>RESULT 2</p>				
<p>AAB82676</p>				
ID	AAB82676	standard,	protein,	419 AA.
XX	AAB82676;			
AC	15-OCT-2001	(first entry)		
DT				
XX				
DE	Human protein C derivative (S11G/Q32E/N33D/L194S/T254S).			
XX	Protein C; human; coronary syndrome; thrombosis; angina;			
KW	myocardial infarction; vascular occlusive disorder; hypercoagulation;			
KW	sepsis; protein C deficiency; occlusion; thromboembolism; stenosis;			
KW	antibacterial; immunosuppressive; thrombolytic; cardiac; antianginal;			
KW	anticoagulant; therapy; mutant; mutein.			
XX				
OS	Homo sapiens.			
XX	Synthetic.			
XX				
EH	Key	Location/Qualifiers		
FT	Domain	1..45		
FT		/note= "Gla domain"		
FT	Modified-site	6		
FT		/note= "gamma-carboxylated"		
FT	Modified-site	7		
FT		/note= "gamma-carboxylated"		
FT	Misc-difference	11		
FT		/note= "Ser in wild-type protein"		
FT	Modified-site	14		
FT		/note= "gamma-carboxylated"		
FT	Modified-site	16		
FT		/note= "gamma-carboxylated"		
FT	Modified-site	19		
FT		/note= "gamma-carboxylated"		
FT	Modified-site	20		
FT		/note= "gamma-carboxylated"		
FT	Modified-site	25		
FT		/note= "gamma-carboxylated"		
FT	Modified-site	26		
FT		/note= "gamma-carboxylated"		
FT	Modified-site	29		
FT		/note= "N-glycosylated"		
FT	Misc-difference	32		
FT		/note= "Gln in wild-type protein"		
FT	Misc-difference	33		
FT		/note= "Asn in wild-type protein"		
FT	Disulfide-bond	50..69		
FT		59..64		
FT	Disulfide-bond	80..89		
FT		98..109		
FT	Disulfide-bond	120..133		
FT		141..177		
FT	Disulfide-bond	155..157		
FT		/note= "cleavage makes a 2-chain inactive precursor (155-amino acid light chain attached via a disulfide bond to a 263-amino acid heavy chain)"		
FT	Peptide	158..169		
FT		/note= "activation peptide; removal activates the 2-chain zymogen"		
FT	Cleavage-site	169..170		
FT		/note= "thrombin cleavage site"		

FT	Misc-difference	194	/note= "Ileu in wild-type protein"
FT	Disulfide-bond	196	.212
FT	Modified-site	248	/note= "N-glycosylated"
FT	Misc-difference	254	/note= "Thr in wild-type protein"
FT	Modified-site	313	/note= "N-glycosylated"
FT	Modified-site	329	/note= "N-glycosylated"
FT	Disulfide-bond	331	.345
FT	Disulfide-bond	356	.384
XX			
XX	WO200157193-A2.		
XX			
XX	09-AUG-2001.		
XX			
XX	19-JAN-2001; 2001WO-US000020.		
XX			
XX	02-FEB-2000; 2000US-0179801P.		
XX	14-MAR-2000; 2000US-0189197P.		
XX			
XX	(ELIL) LILLY & CO ELI.		
XX			
XX	Gerlitz BE, Jones BE;		
XX	WPI; 2001-496919/54.		
XX	N-PSDB; AAB26364.		
XX			
XX	Novel human protein C derivative for treating, e.g., myocardial		
XX	infarction, unstable angina, sepsis, thrombotic disorders, acute arterial		
XX	thrombotic occlusion, and thrombolism.		
XX			
XX	Claim 4; Page 53-54; 63pp; English.		
XX			
XX	The present sequence is that of a claimed human protein C derivative in		
XX	which Ser at position 11 of the mature wild-type protein C sequence (see		
XX	AAB82673) is substituted with Gly, Gln at position 32 with Glu, Asn at		
XX	position 33 with Asp, Leu at position 194 with Ser, and Thr at position		
XX	254 with Ser. It is an example of protein C derivatives of the invention		
XX	that have at least 2 amino acid substitutions, but which have increased		
XX	anticoagulant activity and resistance to inactivation by serpin compared		
XX	with the wild-type protein, while retaining the biological activity of		
XX	the wild-type protein. A method of producing the derivatives using		
XX	recombinant DNA methods is claimed. The protein C derivatives are useful		
XX	for treating coronary syndromes and disease states predisposing to		
XX	thrombosis (e.g. myocardial infarction and unstable angina), vascular		
XX	occlusive disorders and hypercoagulable states, sepsis (in combination		
XX	with bactericidal permeability increasing protein or with tissue factor		
XX	pathway inhibitor), thrombotic disorders (in combination with an anti-		
XX	platelet agent or by local delivery through an intracoronary catheter),		
XX	protein C deficiency, acute arterial thrombotic occlusion,		
XX	thromboembolism, or stenosis in coronary, cerebral or peripheral arteries		
XX	or in vascular grafts. Human patients with genetically predisposed		
XX	prothrombotic disorders may be treated by gene therapy (all claimed)		
XX			
XX	Sequence 419 AA;		
XX			
XX	Query Match	88.9%;	Score 176; DB 4; Length 419;
XX	Best Local Similarity	77.3%;	Pred. No. 1.9e-20;
XX	Matches 34; Conservative	0;	Mismatches 10; Indels 0; Gaps 0;
XX			
XX	1 ANSFLXXLRHSSLRXCITXICDPFKXKXIFEDVDITLAWSGH 44		
XX	1 ANSFLELRHGSLEKRECIIEICDPEAKEIFEDVDITLAWSGH 44		
XX			
XX	RESULT 3		
XX	AAB82675		
XX	ID AAB82675 standard; protein; 419 AA.		
XX			
XX	AAB82675;		

XX 15-OCT-2001 (first entry)
 DT
 XX
 DE Human protein C derivative (S11G/Q32E/N35D/L194S).
 XX
 XX Protein C; human; coronary syndrome; thrombosis; angina;
 KM myocardial infarction; vascular occlusive disorder; hypercoagulation;
 KM sepsis; protein C deficiency; occlusion; thromboembolism; stenosis;
 KM antibacterial; immunosuppressive; thrombolytic; cardiac; antiangiinal;
 KM anticoagulant; therapy; mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key
 FT Domain
 FT Location/Qualifiers
 FT 1..45
 FT /note= "Gla domain"
 FT Modified-site
 FT 6 /note= "gamma-carboxylated"
 FT Modified-site
 FT 7 /note= "gamma-carboxylated"
 FT Modified-site
 FT 11 /note= "gamma-carboxylated"
 FT Misc-difference
 FT 14 /note= "Ser in wild-type protein"
 FT Modified-site
 FT 16 /note= "gamma-carboxylated"
 FT Modified-site
 FT 19 /note= "gamma-carboxylated"
 FT Modified-site
 FT 20 /note= "gamma-carboxylated"
 FT Modified-site
 FT 25 /note= "gamma-carboxylated"
 FT Modified-site
 FT 26 /note= "gamma-carboxylated"
 FT Modified-site
 FT 29 /note= "gamma-carboxylated"
 FT Modified-site
 FT 32 /note= "N-glycosylated"
 FT Misc-difference
 FT 33 /note= "Gln in wild-type protein"
 FT Misc-difference
 FT 50..69 /note= "Asn in wild-type protein"
 FT Disulfide-bond
 FT 59..64
 FT Disulfide-bond
 FT 80..89
 FT Disulfide-bond
 FT 98..109
 FT Disulfide-bond
 FT 120..133
 FT Disulfide-bond
 FT 141..277
 FT Disulfide-bond
 FT 156..157
 FT Cleavage-site
 FT /note= "cleavage makes a 2-chain inactive precursor (155-
 amino acid light chain attached via a disulfide bond to a
 262-amino acid heavy chain)"
 FT
 FT Peptide
 FT 158..169
 FT /note= "activation peptide; removal activates the 2-chain
 zymogen"
 FT Cleavage-site
 FT 169..170
 FT /note= "thrombin cleavage site"
 FT Misc-difference
 FT 194 /note= "Leu in wild-type protein"
 FT Disulfide-bond
 FT 196..212
 FT Modified-site
 FT 248 /note= "N-glycosylated"
 FT Modified-site
 FT 313 /note= "N-glycosylated"
 FT Modified-site
 FT 329 /note= "N-glycosylated"
 FT /note= "N-glycosylated"
 FT Disulfide-bond
 FT 331..345
 FT Disulfide-bond
 FT 356..384
 XX
 XX WO200157193-A2.
 XX
 XX 09-AUG-2001.
 XX
 XX 19-JAN-2001; 2001WO-US000020.

XX 02-FEB-2000; 2000US-0179901P.
 PR 14-MAR-2000; 2000US-0189197P.
 XX
 XX (EHLI) LILLY & CO ELI.
 XX
 XX Gerlitz BE, Jones BE;
 PI
 XX WPI; 2001-496919/54.
 DR N-PSDB; AAH26363.
 XX
 XX Novel human protein C derivative for treating, e.g., myocardial
 PT infarction, unstable angina, sepsis, thrombotic disorders, acute arterial
 PT thrombotic occlusion, and thromboembolism.
 XX
 XX Claim 3; Page 52-53; 63pp; English.
 XX
 CC The present sequence is that of a claimed human protein C derivative in
 CC which Ser at amino acid position 11 of the mature wild-type protein C
 CC sequence (see AAB82673) is substituted with Gly, Gln at position 33 with
 CC Gln, Asn at position 33 with Asp, and Leu at position 194 with Ser. The
 CC protein is an example of protein C derivatives of the invention that have
 CC at least 2 amino acid substitutions, but which have increased
 CC anticoagulant activity and resistance to inactivation by serpins compared
 CC with the wild-type protein, while retaining the biological activity of
 CC the wild-type protein. A method of producing the derivatives using
 CC recombinant DNA methods is claimed. The protein C derivatives are useful
 CC for treating coronary syndromes and disease states predisposing to
 CC thrombosis (e.g. myocardial infarction and unstable angina), vascular
 CC occlusive disorders and hypercoagulable states, sepsis (in combination
 CC with bactericidal permeability increasing protein or with tissue factor
 CC pathway inhibitor), thrombotic disorders (in combination with an anti-
 CC platelet agent or by local delivery through an intracoronary catheter),
 CC protein C deficiency, acute arterial thrombotic occlusion,
 CC thromboembolism, or stenosis in coronary, cerebral or peripheral arteries
 CC or in vascular grafts. Human patients with genetically predisposed
 CC prothrombotic disorders may be treated by gene therapy (all claimed)
 CC
 XX
 SQ Sequence 419 AA;
 Query Match 88.9%; Score 176; DB 4; Length 419;
 Best Local Similarity 77.3%; Pred. No. 1,9e-20;
 Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 1 ANSELYXLRHSSILKRCIXICDFFXXAKXIFEDVDDTLAFWSKH 44
 Db 1 ANSELYXLRHSSILKRCIXICDFFXXAKXIFEDVDDTLAFWSKH 44
 ID AAE08628 standard; protein; 419 AA.
 AC AAE08628;
 XX
 DT 01-NOV-2001 (first entry)
 XX
 DE Human protein C derivative #2.
 XX
 XX Human; protein C derivative; anticoagulation activity; thrombosis;
 KM sepsin inactivation; acute coronary syndrome; myocardial infarction;
 KM vascular occlusive disorder; hypercoagulable states; angina; sepsis;
 KM disseminated intravascular coagulation; DIC; burn; transplantation;
 KM sickle cell disease; viral haemorrhagic fever; protein C deficiency;
 KM haemolytic uremic syndrome; acute arterial thrombotic occlusion;
 KM thromboembolism; prothrombotic disorder; gene therapy; thalassemia.
 XX
 OS Homo sapiens.
 XX
 XX WO200159084-A1.
 XX
 XX 16-AUG-2001.

PF 02-FEB-2001; 2001MO-US001221.
 XX 11-FEB-2000; 2000US-0181948P.
 PR 14-MAR-2000; 2000US-0189199P.
 XX (ELIL) LILLY & CO ELI.
 PA Gerlitz BE, Grinnell BW, Jones BE;
 PI WPI; 2001-514662/56.
 DR N-PSDB; AAD15225.
 XX
 PT Protein C derivative for treating acute coronary syndromes, vascular
 PT occlusive disorders, thrombotic disorders and sepsis, comprises
 PT substitutions at specified amino acid positions.
 PS Claim 4; Page 47-48; 59pp; English.
 XX
 CC The invention relates to human protein C derivatives and nucleic acid
 CC molecules encoding such derivatives. These derivatives have increased
 CC anticoagulation activity, resistance to serpin inactivation and increased
 CC sensitivity to thrombin activation compared to wild type protein C, and
 CC retains the biological activity of the wild type human protein C. Protein
 CC C derivatives are useful in the manufacture of a medicament for the
 CC treatment of acute coronary syndromes e.g. myocardial infarction and
 CC unstable angina; and disease states predisposing to thrombosis; vascular
 CC occlusive disorders and hypercoagulable states e.g. disseminated
 CC intravascular coagulation (DIC), burns, transplantations, thalassaemia,
 CC sickle cell disease, viral haemorrhagic fever and haemolytic uraemic
 CC syndrome; sepsis in combination with bacterial permeability increasing
 CC protein; thrombotic disorders in combination with an anti-platelet agent;
 CC protein C deficiency; acute arterial thrombotic occlusion;
 CC thromboembolism or stenosis in coronary, cerebral or peripheral arteries
 CC or in vascular grafts in combination with a thrombolytic agent. Nucleic
 CC acid molecules of the invention are useful for treating humans with
 CC genetically predisposed prothrombotic disorders by gene therapy. The
 CC present sequence is human protein C derivative
 SQ Sequence 419 AA;
 Query Match 88.9%; Score 176; DB 4; Length 419;
 Best Local Similarity 77.3%; Pred. No. 1.9e-20;
 Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 1 ANSFLXRLRHSLSKXCIXXICDPFXAXXIFEDVDPTLAFWSKH 44
 DB 1 ANSFLRLRHSLSKXCIXXICDPFXAXXIFEDVDPTLAFWSKH 44
 RESULT 5
 AAE08627
 ID AAE08627 standard; protein; 419 AA.
 XX
 AC AAE08627;
 DT 01-NOV-2001 (first entry)
 XX
 DE Human protein C derivative #1.
 XX
 XX Human; protein C derivative; anticoagulation activity; thrombosis;
 KW serpin inactivation; acute coronary syndrome; myocardial infarction;
 KW vascular occlusive disorder; hypercoagulable state; angina; sepsis;
 KW disseminated intravascular coagulation; DIC; burn; transplantation;
 KW sickle cell disease; viral haemorrhagic fever; protein C deficiency;
 KW haemolytic uraemic syndrome; acute arterial thrombotic occlusion;
 KW thromboembolism; prothrombotic disorder; gene therapy; thalassaemia.
 OS Homo sapiens.
 XX
 XX MO200159084-A1.
 PN 16-AUG-2001.
 XX

PF 02-FEB-2001; 2001MO-US001221.
 XX 11-FEB-2000; 2000US-0181948P.
 PR 14-MAR-2000; 2000US-0189199P.
 XX (ELIL) LILLY & CO ELI.
 PA Gerlitz BE, Grinnell BW, Jones BE;
 PI WPI; 2001-514662/56.
 DR N-PSDB; AAD15225.
 XX
 PT Protein C derivative for treating acute coronary syndromes, vascular
 PT occlusive disorders, thrombotic disorders and sepsis, comprises
 PT substitutions at specified amino acid positions.
 PS Claim 3; Page 46-47; 59pp; English.
 XX
 CC The invention relates to human protein C derivatives and nucleic acid
 CC molecules encoding such derivatives. These derivatives have increased
 CC anticoagulation activity, resistance to serpin inactivation and increased
 CC sensitivity to thrombin activation compared to wild type protein C, and
 CC retains the biological activity of the wild type human protein C. Protein
 CC C derivatives are useful in the manufacture of a medicament for the
 CC treatment of acute coronary syndromes e.g. myocardial infarction and
 CC unstable angina; and disease states predisposing to thrombosis; vascular
 CC occlusive disorders and hypercoagulable states e.g. disseminated
 CC intravascular coagulation (DIC), burns, transplantations, thalassaemia,
 CC sickle cell disease, viral haemorrhagic fever and haemolytic uraemic
 CC syndrome; sepsis in combination with bacterial permeability increasing
 CC protein; thrombotic disorders in combination with an anti-platelet agent;
 CC protein C deficiency; acute arterial thrombotic occlusion;
 CC thromboembolism or stenosis in coronary, cerebral or peripheral arteries
 CC or in vascular grafts in combination with a thrombolytic agent. Nucleic
 CC acid molecules of the invention are useful for treating humans with
 CC genetically predisposed prothrombotic disorders by gene therapy. The
 CC present sequence is human protein C derivative
 SQ Sequence 419 AA;
 Query Match 88.9%; Score 176; DB 4; Length 419;
 Best Local Similarity 77.3%; Pred. No. 1.9e-20;
 Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 1 ANSFLXRLRHSLSKXCIXXICDPFXAXXIFEDVDPTLAFWSKH 44
 DB 1 ANSFLRLRHSLSKXCIXXICDPFXAXXIFEDVDPTLAFWSKH 44
 RESULT 6
 AAE08629
 ID AAE08629 standard; protein; 419 AA.
 XX
 AC AAE08629;
 DT 01-NOV-2001 (first entry)
 XX
 DE Human protein C derivative #3.
 XX
 XX Human; protein C derivative; anticoagulation activity; thrombosis;
 KW serpin inactivation; acute coronary syndrome; myocardial infarction;
 KW vascular occlusive disorder; hypercoagulable state; angina; sepsis;
 KW disseminated intravascular coagulation; DIC; burn; transplantation;
 KW sickle cell disease; viral haemorrhagic fever; protein C deficiency;
 KW haemolytic uraemic syndrome; acute arterial thrombotic occlusion;
 KW thromboembolism; prothrombotic disorder; gene therapy; thalassaemia.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 PH Misc-difference 10 /note="Encoded by CAA"
 FT
 FT

PN W0200159084-A1.
 XX 16-AUG-2001.
 XX 02-FEB-2001; 2001MO-US001221.
 XX 11-FEB-2000; 2000US-0181948P.
 PR 14-MAR-2000; 2000US-0189199P.
 XX (ELIL) LILLY & CO ELI.
 PA Gerilitz BE, Grinnell BW, Jones BE;
 PI WPI; 2001-514662/56.
 DR N-PSDB; AADI5227.
 XX Protein C derivative for treating acute coronary syndromes, vascular
 PT occlusive disorders, thrombotic disorders and sepsis, comprises
 PT substitutions at specified amino acid positions.
 PS Claim 5; Page 48-49; 59pp; English.
 XX The invention relates to human protein C derivatives and nucleic acid
 CC molecules encoding such derivatives. These derivatives have increased
 CC anticoagulation activity, resistance to serpin inactivation and increased
 CC sensitivity to thrombin activation compared to wild type protein C, and
 CC retains the biological activity of the wild type human protein C. Protein
 CC derivatives are useful in the manufacture of a medicament for the
 CC treatment of acute coronary syndromes e.g. myocardial infarction and
 CC unstable angina; and disease states predisposing to thrombosis; vascular
 CC occlusive disorders and hypercoagulable states e.g. disseminated
 CC intravascular coagulation (DIC), burns, transplantations, thalassaemia,
 CC sickle cell disease, viral haemorrhagic fever and haemolytic uremic
 CC syndrome; sepsis in combination with bacterial permeability increasing
 CC protein; thrombotic disorders in combination with an anti-platelet agent;
 CC thromboembolism or stenosis in coronary, cerebral or peripheral arteries
 CC or in vascular grafts in combination with a thrombolytic agent. Nucleic
 CC acid molecules of the invention are useful for creating humans with
 CC genetically predisposed prothrombotic disorders by gene therapy. The
 CC present sequence is human protein C derivative
 SQ Sequence 419 AA;
 QY Query Match 88.9%; Score 176; DB 4; Length 419;
 DB Best Local Similarity 77.3%; Pred. No. 1.9e-20;
 Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 1 ANSFLXXLRHSSLSRXICIXXICDFXXAXXIFEDVDTTAFWSKH 44
 1 ANSFLLELRHGSLEKICIERICDFEAKXIFEDVDTTAFWSKH 44
 RESULT 7
 ID ABB79950 standard; protein; 45 AA.
 XX ABB79950;
 AC ABB79950;
 DT 12-DEC-2002 (first entry)
 XX Human protein C mutated Glu domain SED.
 DB Human protein C mutated Glu domain SED.
 XX Protein C; Glu domain; human; blood clotting; anticoagulant;
 KM thrombolytic; antiarteriosclerotic; cardiac; antiaggregant; mutant;
 XX mutein.
 OS Homo sapiens.
 OS Synthetic.
 XX Key Location/Qualifiers
 FT Msc-difference 23 /note= "wild-type Asp substituted by Ser"
 FT

FT Msc-difference 32 /note= "wild-type Glu substituted by Glu"
 FT Msc-difference 33 /note= "wild-type Asn substituted by Asp"
 FT /note= "wild-type Asp substituted by Asp"
 PN W0200270681-A1.
 XX 12-SEP-2002.
 PD 01-MAR-2002; 2002MO-SE000363.
 XX 02-MAR-2001; 2001US-0272466P.
 XX (TACT-) TAC THROMBOSIS & COAGULATION AB.
 PA Dahlback B;
 PI WPI; 2002-713449/77.
 DR New variant blood coagulation component, useful for manufacturing a
 PT medicament for treating or preventing coagulation disorders, e.g.
 PT thrombosis, comprises an anticoagulant activity in the protein C-
 PT anticoagulant system of blood.
 PS Example 1; Page; 56pp; English.
 XX The present sequence is the protein sequence of a mutated Glu domain (N-
 CC terminal amino acids 1-45) of human protein C. The mutated Glu domain
 CC contains the substitution mutations D23S, Q32E and N33D. Protein C and
 CC activated protein C variants comprising a mutated Glu domain are provided
 CC by the invention. The variants contain at least 6, and optionally 7-10,
 CC amino acid substitutions. A preferred mutant (designated QGNSBDV, see
 CC ABB79946) has the mutations H10Q, S11G, S12N, D23S, Q32E, N33D and H44Y,
 CC and shows greatly enhanced anticoagulant activity in standard in vitro
 CC coagulation assays. The present mutant (designated SED) was produced in
 CC an example from the invention as a step toward the production of the
 CC QGNSBDV mutant Glu domain, and shows little, if any, improvement in
 CC anticoagulant activity over wild-type activated protein C. The invention
 CC provides methods for producing the variants based on DNA technology, and
 CC with the use of the variants for the treatment of coagulation disorders
 CC such as thrombosis or Aic resistance, or in diagnostic test systems for
 CC assaying components of the protein C-anticoagulant system (all claimed).
 CC The variants may also be used in treating arteriosclerosis, myocardial
 CC infarction, and disseminated intravascular coagulation. Note: The present
 CC sequence is not shown in the specification but is derived from the human
 CC wild-type Glu domain sequence given on page 7 of the specification (see
 CC ABB79947)
 SQ Sequence 45 AA;
 QY Query Match 87.9%; Score 174; DB 5; Length 45;
 DB Best Local Similarity 77.3%; Pred. No. 3.6e-21;
 Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 1 ANSFLXXLRHSSLSRXICIXXICDFXXAXXIFEDVDTTAFWSKH 44
 1 ANSFLLELRHSSLEKICIERICDFEAKXIFEDVDTTAFWSKH 44
 RESULT 8
 ID AAY18299 standard; peptide; 44 AA.
 XX AAY18299;
 AC AAY18299;
 DT 17-AUG-1999 (first entry)
 XX Modified Glu domain of vitamin K-dependent protein.
 DB Glu domain; mutein; vitamin K-dependent protein; clotting disorder;
 XX therapy.
 KM Homo sapiens.
 XX

OS Synthetic.
 XX Key Location/Qualifiers
 FT Misc-difference 1..44
 FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic
 FT acid"
 XX
 XX
 PN WO9920767-A1.
 XX
 XX 29-APR-1999.
 PD
 XX 20-OCT-1998; 98WO-US022152.
 PF
 XX 23-OCT-1997; 97US-00955636.
 PR
 XX (MINU) UNIV MINNESOTA.
 XX
 XX Nelasetuen GL;
 PI
 XX WPI, 1999-288309/24.
 DR
 XX
 XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid
 PT domain, useful for treating clotting disorders.
 XX
 XX Claim 8, Page 78; 86pp; English.
 PS
 XX This sequence represents a modified GLA (gamma-carboxyglutamic acid)
 CC domain. The invention relates to a vitamin K-dependent polypeptide
 CC comprising a modified GLA domain containing an amino acid substitution
 CC which enhances membrane binding of the modified polypeptide as compared
 CC to the native polypeptide. The polypeptide is used to treat a clotting
 CC disorder by decreasing or increasing clot formation. Modification of the
 CC GLA domain results in a protein which has enhanced membrane binding
 CC affinity as compared to the native protein
 CC
 SQ Sequence 44 AA;
 Query Match 86.9%; Score 172; DB 2; Length 44;
 Best Local Similarity 97.7%; Pred. No. 7,6e-21;
 Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ANSFLXKLRHSLKRXKXICDFXXAKXIFEDVDTLAFWSKH 44
 DB 1 ANSFLXKLRHSLKRXKXICDFXXAKXIFEDVDTLAFWSKH 44
 RESULT 9
 ID AAY18309 standard; peptide; 44 AA.
 XX
 XX AAY18309;
 AC
 XX 17-AUG-1999 (first entry)
 DT
 XX Modified GLA domain of vitamin K-dependent protein.
 DE
 XX GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
 KM therapy.
 KM
 XX Homo sapiens.
 OS
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FT Misc-difference 1..44
 FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic
 FT acid"
 XX
 XX WO9920767-A1.
 PN
 XX 29-APR-1999.
 PD
 XX 20-OCT-1998; 98WO-US022152.
 PF
 XX

PR 23-OCT-1997; 97US-00955636.
 XX
 XX (MINU) UNIV MINNESOTA.
 XX
 XX Nelasetuen GL;
 PI
 XX WPI, 1999-288309/24.
 DR
 XX
 XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid
 PT domain, useful for treating clotting disorders.
 XX
 XX Disclosure; Page 79-80; 86pp; English.
 PS
 XX This sequence represents a modified GLA (gamma-carboxyglutamic acid)
 CC domain. The invention relates to a vitamin K-dependent polypeptide
 CC comprising a modified GLA domain containing an amino acid substitution
 CC which enhances membrane binding of the modified polypeptide as compared
 CC to the native polypeptide. The polypeptide is used to treat a clotting
 CC disorder by decreasing or increasing clot formation. Modification of the
 CC GLA domain results in a protein which has enhanced membrane binding
 CC affinity as compared to the native protein
 CC
 SQ Sequence 44 AA;
 Query Match 86.9%; Score 172; DB 2; Length 44;
 Best Local Similarity 97.7%; Pred. No. 7,6e-21;
 Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ANSFLXKLRHSLKRXKXICDFXXAKXIFEDVDTLAFWSKH 44
 DB 1 ANSFLXKLRHSLKRXKXICDFXXAKXIFEDVDTLAFWSKH 44
 RESULT 10
 ID AAY18298 standard; peptide; 44 AA.
 XX
 XX AAY18298;
 AC
 XX 17-AUG-1999 (first entry)
 DT
 XX Modified GLA domain of vitamin K-dependent protein.
 DE
 XX GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
 KM therapy.
 KM
 XX Homo sapiens.
 OS
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FT Misc-difference 1..44
 FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic
 FT acid"
 XX
 XX WO9920767-A1.
 PN
 XX 29-APR-1999.
 PD
 XX 20-OCT-1998; 98WO-US022152.
 PF
 XX 23-OCT-1997; 97US-00955636.
 PR
 XX (MINU) UNIV MINNESOTA.
 XX
 XX Nelasetuen GL;
 PI
 XX WPI, 1999-288309/24.
 DR
 XX
 XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid
 PT domain, useful for treating clotting disorders.
 XX
 XX Claim 7, Page 78; 86pp; English.

CC This sequence represents a modified GLA (gamma-carboxyglutamic acid) domain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution CC which enhances membrane binding of the modified polypeptide as compared CC to the native polypeptide. The polypeptide is used to treat a clotting CC disorder by decreasing or increasing clot formation. Modification of the CC GLA domain results in a protein which has enhanced membrane binding CC affinity as compared to the native protein

XX
SQ Sequence 44 AA;

Query Match 86.9%; Score 172; DB 2; Length 44;
Best Local Similarity 97.7%; Pred. No. 7, 6e-21;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANSFLXXLRHSSLRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
Db 1 ANSFLXXLRHSSLRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44

RESULT 11
AA18303

ID AAY18303 standard; peptide; 44 AA.

XX
AC AAY18303;

DT 17-APR-1999 (first entry)

XX
DE Human protein C GLA domain.

XX
KW GLA domain; vitamin K-dependent protein; clotting disorder; therapy.

XX
OS Homo sapiens.

XX
FH Key Location/Qualifiers

FT MISC-difference 1..44
FT /note="Xaa= gamma-carboxyglutamic acid, or glutamic
FT acid"

XX
PV WO9920767-A1.

XX
PD 29-APR-1999.

XX
PF 20-OCT-1998; 98WO-US022152.

XX
PR 23-OCT-1997; 97US-00955636.

XX
PA (MINU) UNIV MINNESOTA.

XX
PI Nelsestuen GL;

XX
DR WPI; 1999-288309/24.

XX
PT Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid
XX domain, useful for treating clotting disorders.

XX
PS Disclosure; Page 14; 86pp; English.

XX
CC This sequence is the protein C GLA (gamma-carboxyglutamic acid) domain.
CC The invention relates to a vitamin K-dependent polypeptide comprising a
CC modified GLA domain containing an amino acid substitution which enhances
CC membrane binding of the modified polypeptide as compared to the native
CC polypeptide. The polypeptide is used to treat a clotting disorder by
CC decreasing or increasing clot formation. Modification of the GLA domain
CC results in a protein which has enhanced membrane binding affinity as
CC compared to the native protein

XX
SQ Sequence 44 AA;

Query Match 86.9%; Score 172; DB 2; Length 44;
Best Local Similarity 95.5%; Pred. No. 7, 6e-21;
Matches 42; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANSFLXXLRHSSLRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
Db 1 ANSFLXXLRHSSLRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44

RESULT 12

ID AAB36402 standard; peptide; 44 AA.

XX
AC AAB36402;

DT 27-FEB-2001 (first entry)

XX
DE Human protein C gamma-carboxyglutamic acid domain SEQ ID NO:1.

XX
KW Vitamin K-dependent protein; factor VII; protein C; GLA domain;
KW gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;
KW factor X; prothrombin; enhanced membrane binding affinity;
KW clot formation; thrombolytic; haemostatic; bleeding disorder; thrombosis;
KW clotting disorder; haemophilia A; haemophilia B; liver disease.

XX
OS Homo sapiens.

XX
PN WO200066753-A2.

XX
PD 09-NOV-2000.

XX
PF 28-APR-2000; 2000WO-US011416.

XX
PR 29-APR-1999; 99US-00302239.

XX
PA (MINU) UNIV MINNESOTA.

XX
PI Nelsestuen GL;

XX
DR WPI; 2001-007226/01.

XX
PT Novel vitamin K-dependent polypeptide useful for treating clotting
XX disorders such as thrombosis and hemophilia, comprises modified gamma-
XX carboxy glutamic acid domain that enhances membrane binding affinity.

XX
PS Example 5; Page 42; 81pp; English.

XX
CC The present invention describes a vitamin K-dependent polypeptide (I)
CC comprising a modified gamma-carboxy glutamic acid (GLA) domain having at
CC least one amino acid substitution, that enhances membrane binding
CC affinity and the activity of the polypeptide relative to a corresponding
CC native vitamin K-dependent polypeptide and inhibits clot formation. (II)
CC can have thrombolytic and haemostatic activities, and can be used as an
CC inhibitor of clot formation. (II) is useful for decreasing clot formation
CC in a mammal, a factor VII or factor IX containing a modified GLA domain
CC is useful for increasing clot formation and for treating a bleeding
CC disorder including thrombosis and clotting disorders such as haemophilia
CC A, haemophilia B and liver disease. The present sequence represents a
CC human protein C GLA domain sequence, given in the exemplification of the
XX present invention

XX
SQ Sequence 44 AA;

Query Match 86.9%; Score 172; DB 4; Length 44;
Best Local Similarity 95.5%; Pred. No. 7, 6e-21;
Matches 42; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANSFLXXLRHSSLRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
Db 1 ANSFLXXLRHSSLRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44

RESULT 13

ID ADD50094 standard; protein; 44 AA.

XX
AC ADD50094;

XX 15-JAN-2004 (first entry)
 DT Human vitamin K-dependent protein #1.
 DE Human, vitamin K-dependent protein; gamma-carboxyglutamic acid domain;
 XX GLA domain; membrane binding affinity; clot formation; haemophilia;
 KM clotting disorder; site directed mutagenesis; haemostatic; anticoagulant;
 XX thrombolytic.
 OS Homo sapiens.
 XX US2003100506-A1.
 PN 29-MAY-2003.
 PD 18-NOV-2002; 2002US-00298330.
 PF 23-OCT-1997; 97US-00955636.
 XX 29-APR-1998; 98US-00302239.
 PR 03-FEB-2000; 2000US-00497591.
 XX (NEUS/) NEUSESTUEN G L.
 PA Nelesten GL;
 PI WPI: 2003-606646/57.
 DR New vitamin K-dependent polypeptide for modulating clot formation in
 PT mammals comprises a modified gamma-carboxyglutamic acid domain that
 PT enhances membrane binding affinity and activity of the polypeptide.
 XX Example 5; SEQ ID NO 1; 51pp; English.
 PS The invention relates to a vitamin K-dependent polypeptide comprising a
 CC modified gamma-carboxyglutamic acid (GLA) domain that enhances membrane
 CC binding affinity and activity of the polypeptide relative to a
 CC corresponding native vitamin K-dependent polypeptide, where the modified
 CC GLA domain comprises a glutamic acid residue at position 34. The
 CC polypeptide is useful in modulating clot formation in mammals or in
 CC treating certain types of haemophilia or clotting disorders. The membrane
 CC binding affinity of polypeptides is increased by site directed
 CC mutagenesis in the GLA domain. This sequence represents a vitamin K-
 CC dependent protein of the invention.
 SO Sequence 44 AA;
 QY Query Match 86.9%; Score 172; DB 7; Length 44;
 DB Best Local Similarity 95.5%; Pred. No. 7, 6e-21;
 1 ANSFLXLRHSSILRXICIXICDPFXAKXIFEDVDDTLAFWSKH 44
 1 ANSFLXLRHSSILRXICIXICDPFXAKXIFQNDVDTLAFWSKH 44
 DE Partial human protein C amino acid sequence.
 DE Gamma carboxyglutamic acid; human protein C; GLA domain; chimera;
 KM PRC/RSV; RSV-PC; amplification; PCR; primer; transfection; anticoagulant;
 KM human 293 cells; myocardial infarction; venous thrombosis;
 KM disseminated intravascular coagulation; thromboembolic disease; lupus;
 KM adult respiratory distress syndrome; factor V Leiden; stroke.
 XX Homo sapiens.
 OS

XX Key Location/Qualifiers
 PH Misc-difference 6 /note= "Gamma carboxyglutamic acid"
 FT Misc-difference 7 /note= "Gamma carboxyglutamic acid"
 FT Misc-difference 14 /note= "Gamma carboxyglutamic acid"
 FT Misc-difference 16 /note= "Gamma carboxyglutamic acid"
 FT Misc-difference 19 /note= "Gamma carboxyglutamic acid"
 FT Misc-difference 20 /note= "Gamma carboxyglutamic acid"
 FT Misc-difference 25 /note= "Gamma carboxyglutamic acid"
 FT Misc-difference 26 /note= "Gamma carboxyglutamic acid"
 FT Misc-difference 29 /note= "Gamma carboxyglutamic acid"
 FT Misc-difference 29 /note= "Gamma carboxyglutamic acid"
 PN WO982018-A1.
 PD 14-MAY-1998.
 PF 07-NOV-1997; 97WO-US020376.
 XX 08-NOV-1996; 96US-00745254.
 PR 25-JUL-1997; 97US-0053768P.
 XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.
 PA Esmen CT, Smitrov M;
 PI WPI: 1998-286934/25.
 DR Protein C chimeric proteins for use as anticoagulants - having gamma
 XX carboxyglutamic acid region replaced with Vitamin K dependent clotting
 PT factor e.g. prothrombin.
 PS Example 1; Page 15; 42pp; English.
 CC The present sequence represents the first three exons of the human
 CC protein C protein, which contains gamma carboxyglutamic acid modified
 CC residues. This sequence was replaced with the corresponding regions of
 CC modified human prothrombin (AAW75709), to create a protein C prothrombin
 CC GLA domain chimera. To produce this chimera, the wild-type protein C cDNA
 CC was ligated into pRC/RSV to form RSV-PC, and then was digested with
 CC restriction enzymes to remove the first three exons and the first codon
 CC of exon four. The prothrombin cDNA was amplified, digested, and then
 CC ligated into RSV-PC at the identical site where the protein C cDNA exons
 CC 1-3 had been removed. This construct was then transfected into human 293
 CC cells, from which the chimeric protein can be purified. This chimeric
 CC protein can be used as an anticoagulant, to treat disorders where protein
 CC 5 is low, some forms of lupus, following stroke or myocardial infarction,
 CC after venous thrombosis and in disseminated intravascular coagulation,
 CC adult respiratory distress syndrome, in thromboembolic disease or factor
 CC V Leiden
 SO Sequence 45 AA;
 QY Query Match 86.9%; Score 172; DB 2; Length 45;
 DB Best Local Similarity 95.5%; Pred. No. 7, 8e-21;
 1 ANSFLXLRHSSILRXICIXICDPFXAKXIFEDVDDTLAFWSKH 44
 1 ANSFLXLRHSSILRXICIXICDPFXAKXIFQNDVDTLAFWSKH 44
 DE Partial human protein C amino acid sequence.
 DE Gamma carboxyglutamic acid; human protein C; GLA domain; chimera;
 KM PRC/RSV; RSV-PC; amplification; PCR; primer; transfection; anticoagulant;
 KM human 293 cells; myocardial infarction; venous thrombosis;
 KM disseminated intravascular coagulation; thromboembolic disease; lupus;
 KM adult respiratory distress syndrome; factor V Leiden; stroke.
 XX Homo sapiens.
 OS

XX ABB79947;
AC
XX
DT 12-DEC-2002 (first entry)
XX
DE Human protein C Gla domain.
XX
KW Protein C; Gla domain; human; blood clotting; anticoagulant;
XX thrombolytic; antiarteriosclerotic; cardiant; antiagregant.
XX
OS Homo sapiens.
XX
PN MO200270681-A1.
XX
PD 12-SEP-2002.
XX
PF 01-MAR-2002; 2002WC-SE000363.
XX
PR 02-MAR-2001; 2001US-027246P.
XX
PA (TACT-) TAC THROMBOSIS & COAGULATION AB.
XX
PI Dahlback B;
XX
DR WPI; 2002-713449/77.
XX
PT New variant blood coagulation component, useful for manufacturing a
PT medicament for treating or preventing coagulation disorders, e.g.
PT thrombosis, comprises an anticoagulant activity in the protein C-
PT anticoagulant system of blood.
XX
PS Disclosure; Page 7; 58p; English.
XX
XX The present sequence is the protein sequence of the Gla domain (N-
CC terminal amino acids 1-45) of human protein C. The invention provides
CC human protein C and activated protein C variants in which the Gla domain
CC contains at least 6, and optionally 7-10, amino acid substitutions
CC preferably the substitution mutations H10Q, S11G, S12N, D23S, Q22S, N33D
CC and H44Y (see ABB79946). Protein C variants comprising the mutated Gla
CC domain show much enhanced anticoagulant activity, as shown in increased
CC clotting time in standard in vitro coagulation assays, as a result of
CC enhanced calcium and/or membrane binding properties. The invention
CC provides methods for producing the variants based on DNA technology, and
CC for using the variants in the treatment of coagulation disorders such as
CC thrombosis or APC resistance, or in diagnostic test systems for assaying
CC components of the protein C-anticoagulant system (all claimed). The
CC variants may also be used in treating arteriosclerosis, myocardial
CC infarction, and disseminated intravascular coagulation
XX
SQ Sequence 45 AA;

Query Match 86.9%; Score 172; DB 5; Length 45;
Best Local Similarity 75.0%; Pred. No. 7.8e-21;
Matches 33; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 ANSFLXXLRSSLSRXCIIXICDFFXXXXIFEDVDDTLAFWSKH 44
DB 1 ANSFLSELRRSSLSRECIIEICDFFBKAKEIFQVDDTLAFWSKH 44

Search completed: March 1, 2004, 10:01:23
Job time : 52 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2004, 09:59:33 ; Search time 13.5 Seconds
(without alignments)
313.513 Million cell updates/sec

Title: SEQ1-32GLU-33ASP

Perfect score: 198

Sequence: 1 ANSFLXLRHSLXRCIXX.....XXAKXIFedVDDTLAFWSKH 44

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR 78:**

1: PIR1:**

2: PIR2:**

3: PIR3:**

4: PIR4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	172	86.9	461	1 KXHU	protein C (activat
2	133	67.2	461	1 JX0210	protein C (activat
3	132	66.7	461	1 S18994	protein C (activat
4	115	58.1	456	1 KXBO	protein C (activat
5	107	54.0	482	1 EXRT	coagulation factor
6	103	52.0	492	1 EXBO	coagulation factor
7	102	51.5	488	1 EXHU	coagulation factor
8	94	47.5	443	2 I46932	coagulation factor
9	92	46.5	466	1 KFHU7	coagulation factor
10	78.5	39.6	617	2 S10511	thrombin (EC 3.4.2
11	78.5	39.6	618	2 A35827	thrombin (EC 3.4.2
12	78	39.4	407	1 KFB07	coagulation factor
13	76	38.4	622	1 TBHU	thrombin (EC 3.4.2
14	75	37.9	475	1 EXCH	coagulation factor
15	74	37.4	642	2 S33434	plasma protein S p
16	74	37.4	676	1 KXHU5	plasma protein S p
17	73	36.9	452	1 A30351	coagulation factor
18	73	36.9	459	2 J00419	coagulation factor
19	73	36.9	646	2 S38819	plasma protein S -
20	72	36.4	675	1 KXBO5	plasma protein S p
21	70	35.4	675	1 KXHU5	plasma protein S p
22	69	34.8	461	1 KFHU5	coagulation factor
23	67	33.8	642	2 S33433	plasma protein S p
24	66	33.3	416	1 KFB0	coagulation factor
25	64	32.3	625	1 TBBO	thrombin (EC 3.4.2
26	63	31.8	675	1 KXWSS	plasma protein S p
27	61.5	31.1	396	1 KXBOZ	plasma protein Z -
28	57.5	29.0	422	1 KXHUZ	plasma protein Z p
29	56.5	28.5	594	2 D84859	probable MAP kinas

RESULT 1

KXHU

protein C (activated) (EC 3.4.21.69) precursor - human

N;Alternate names: autoprothrombin IIA; plasma protein C

C;Species: Homo sapiens (man)

C;Date: 17-Mar-1987 #sequence revision 17-Mar-1987 #text_change 16-Jul-1999

C;Accession: A22331; A25426; A21781; A23789; A00927

R;Poster, D.C.; Yoshitake, S.; Davie, E.W.

Proc. Natl. Acad. Sci. U.S.A. 82, 4673-4677, 1985

A;Title: The nucleotide sequence of the gene for human protein C.

A;Reference number: A22331; MUID:85270390; PMID:2991887

A;Accession: A22331

A;Molecule type: DNA

A;Residues: 1-461 <POS>

A;Cross-references: GB:M11228; NID:gl90333; PIDN:AAA60166.1; PID:gl90334

R;Plutsky, J.; Hoskins, J.A.; Long, G.L.; Crabtree, G.R.

Proc. Natl. Acad. Sci. U.S.A. 83, 546-550, 1986

A;Title: Evolution and organization of the human protein C gene.

A;Reference number: A25426; MUID:86120978; PMID:3511471

A;Accession: A25426

A;Molecule type: DNA

A;Residues: 1-445, 'L', 446-461 <PLU>

A;Cross-references: GB:M12712; NID:gl90330; PIDN:AAA60165.1; PID:gl90332

R;Poster, D.; Davie, E.W.

Proc. Natl. Acad. Sci. U.S.A. 81, 4766-4770, 1984

A;Title: Characterization of a cDNA coding for human protein C.

A;Reference number: A21781; MUID:84272714; PMID:6589623

A;Accession: A21781

A;Molecule type: mRNA

A;Residues: 'Q', 107-461 <FOS2>

A;Cross-references: GB:X02059; NID:gl90322; PIDN:AAA60164.1; PID:gl90323

R;Beckmann, R.J.; Schmidt, R.J.; Santerre, R.F.; Plutsky, J.; Crabtree, G.R.; Long, G.L.

Nucleic Acids Res. 13, 5233-5247, 1985

A;Title: The structure and evolution of a 461 amino acid human protein C precursor and it

A;Reference number: A23789; MUID:85269639; PMID:2991859

A;Accession: A23789

A;Molecule type: mRNA

A;Residues: 1-461 <BEC>

A;Cross-references: GB:X02750; NID:G35689; PIDN:CAA26528.1; PID:g763120

R;Miletich, J.P.; Broze Jr., G.J.

J. Biol. Chem. 265, 11397-11404, 1990

A;Title: Beta protein C is not glycosylated at asparagine 329. The rate of translation me

A;Reference number: A4605; MUID:90293094; PMID:1694179

A;Contents: annotation; carbohydrate binding sites; activation peptide

A;Note: the alpha form of protein C is glycosylated at Asn-329, and the beta form is not

R;Harris, R.J.; Ling, V.T.; Spellman, M.W.

J. Biol. Chem. 267, 5102-5107, 1992

A;Title: O-linked fucose is present in the first epidermal growth factor domain of factor

A;Reference number: A4606; MUID:92184750; PMID:1544894

A;Contents: annotation; beta-hydroxyaspartic acid

C;Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that in

activation of factor Va is strongly enhanced by complexing with protein S. Protein C also fa

probable MAP kinas
probable MAP kinas
growth arrest-spec
growth potentiatin
prinosomal replica
growth arrest-spec
protein-tyrosine k
protein-tyrosine k
hypothetical prote
tyrosine kinase re
endothelial kinase
protein-tyrosine k
protein-tyrosine k
vascular endotheli
hypothetical prote
ammonium transport

C;Comment: Protein C is synthesized in the liver as a single chain precursor, which is then, which cleaves a dodecapeptide from the amino end of the heavy chain; this reaction, C;Genetics: A;Gene: GDB:PROC A;Cross-references: GDB:120317; OMIM:176860 A;Map position: 2q33-q21 A;Introns: 24/1; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1 C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology C;Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding F;1-32/Domain: signal sequence #status predicted <SIG> F;27-86/Domain: Gla domain homology <Gla> F;33-42/Domain: propeptide #status predicted <PRO> F;43-197/Domain: protein C light chain #status predicted <LCH> F;92-111/Domain: EGF homology <EG1> F;140-178/Domain: EGF homology <EG2> F;200-461/Domain: protein C heavy chain #status predicted <HCH> F;200-211/Domain: activation peptide #status experimental <APT> F;212-445/Domain: trypsin homology <TRY> F;48-49,56,58,61,62,67,68,71/Modified site: gamma-carboxyglutamic acid (Glu) #status exp F;59-64,92-105,101-120,122-131,140-151,147-160,162-175,183-319,238-254,373-387,398-426/D F;106-111/Disulfide bonds: #status predicted F;110/Binding site: carbohydrate (Thr) (covalent) #status absent F;113/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental F;139,290,355/Binding site: carbohydrate (Asn) (covalent) #status experimental F;211-212/Cleavage site: Arg-Leu (thrombin) #status predicted F;253,299,402/Active site: His, Asp, Ser #status predicted F;371/Binding site: carbohydrate (Asn) (covalent) (partial) #status atypical

Query Match 86.9%; Score 172; DB 1; Length 461;
Best Local Similarity 75.0%; Pred. No. 1e-19;
Matches 33; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 ANSFLLXLRHSLRXICXICDFXXAKXIFEDVDVDTLAFWSKH 44
DB 43 ANSFLEELRHSLEECIEECIECFEAEQIFQNVDDTLAFWSKH 86

RESULT 2

JX0210
Protein C (activated) (EC 3.4.21.69) precursor - mouse
N;Alternate names: vitamin K-dependent serine proteinase
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: JX0210
J;Rada, N.; Sato, M.; Tsujimura, A.; Iwase, R.; Hashimoto-Gotoh, T.
J. Biochem. 111, 491-495, 1992
A;Title: Isolation and characterization of a mouse protein C cDNA.
A;Reference number: JX0210; MUID:92316897; PMID:1618739
A;Accession: JX0210

A;Molecule type: mRNA
A;Residues: 1-461 <KAD>
A;Cross-references: GB:D10445; NID:G220385; PIDN:BAA01235.1; PID:G220386
A;Experimental source: liver
C;Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that re

s.
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglut F;1-33/Domain: signal sequence #status predicted <SIG> F;27-85/Domain: Gla domain homology <Gla> F;34-41/Domain: propeptide #status predicted <PRO> F;42-196/Domain: protein C #status predicted <PRC> F;42-196/Domain: light chain #status predicted <ECL> F;91-130/Domain: EGF homology <EG1> F;139-174/Domain: EGF homology <EG2> F;199-461/Domain: heavy chain #status predicted <PCH> F;199-211/Domain: activation peptide #status predicted <ACT> F;212-461/Domain: vitamin K-dependent serine proteinase #status predicted <VIT> F;212-445/Domain: trypsin homology <TRY> F;47,48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #status F;112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted F;121-130,139-150,146-159,161-174,182-319,238-254,373-387,398-426/Disulfide bonds: #stat F;214,290,355/Binding site: carbohydrate (Asn) (covalent) #status predicted F;253,299,402/Active site: His, Asp, Ser #status predicted

Query Match 67.2%; Score 133; DB 1; Length 461;
Best Local Similarity 56.8%; Pred. No. 2e-13;
Matches 25; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANSFLLXLRHSLRXICXICDFXXAKXIFEDVDVDTLAFWSKH 44
DB 42 ANSFLEELRHSLEECIEECIECFEAEQIFQNVDDTLAFWKY 85

RESULT 3

S18994
Protein C (activated) (EC 3.4.21.69) precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 29-Oct-1999
C;Accession: S18994; S24312
R;Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.
submitted to the EMBL Data Library, February 1992
A;Description: The cDNA cloning and mRNA expression of rat protein C.
A;Reference number: S18994

A;Accession: S18994
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-461 <OKA>
A;Cross-references: EMBL:X64336; NID:G56962; PIDN:CAA45617.1; PID:G56963
R;Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.
Biochim. Biophys. Acta 1131, 329-332, 1992
A;Title: The cDNA cloning and mRNA expression of rat protein C.
A;Reference number: S24312; MUID:92329550; PMID:1627650

A;Accession: S24312
A;Status: preliminary
A;Molecule type: mRNA

A;Residues: 1-461 <OKA2>
A;Cross-references: EMBL:X64336; NID:G56962; PIDN:CAA45617.1; PID:G56963
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology C;Keywords: beta-hydroxyaspartic acid; glycoprotein; hydrolase; serine proteinase F;1-32/Domain: signal sequence #status predicted <SIG> F;27-85/Domain: Gla domain homology <Gla> F;33-42/Domain: propeptide #status predicted <PRO> F;43-461/Domain: protein C #status predicted <PRC> F;91-130/Domain: EGF homology <EG1> F;139-174/Domain: EGF homology <EG2> F;213-445/Domain: trypsin homology <TRY> F;47,48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #status F;112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted F;121-130,139-150,146-159,161-174,182-320,239-255,373-387,398-426/Disulfide bonds: #stat F;215,291,355/Binding site: carbohydrate (Asn) (covalent) #status predicted F;254,300,402/Active site: His, Asp, Ser #status predicted

Query Match 66.7%; Score 132; DB 1; Length 461;
Best Local Similarity 56.8%; Pred. No. 2.9e-13;
Matches 25; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANSFLLXLRHSLRXICXICDFXXAKXIFEDVDVDTLAFWSKH 44
DB 42 ANSFLEELRHSLEECIEECIECFEAEQIFQNVDDTLAFWKY 85

RESULT 4

KXBO

Protein C (activated) (EC 3.4.21.69) precursor - bovine (fragment)
N;Alternate names: autoprothrombin IIA; plasma protein C
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Nov-1980 #sequence_revision 17-Mar-1987 #text_change 16-Jul-1999
C;Accession: A26250; A18385; A18386; A00928
R;Long, G.L.; Balagaje, R.M.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 81, 5653-5656, 1984
A;Title: Cloning and sequence of liver cDNA coding for bovine protein C.
A;Reference number: A26250; MUID:95014826; PMID:6091100
A;Accession: A26250
A;Molecule type: mRNA
A;Residues: 1-456 <LON>
R;Fernlund, P.; Stenflo, J.

J. Biol. Chem. 257, 12170-12179, 1982
A:Title: Amino acid sequence of the light chain of bovine protein C.
A:Reference number: A18385; MUID:83007325; PMID:6896876
A:Accession: A18385
A:Molecule type: protein
A:Residues: 40-194 <PER>
A:Note: 82-Lys was also found
R:Drakenberg, T.; Fernlund, P.; Reepstorff, P.; Stenflo, J.
Proc. Natl. Acad. Sci. U.S.A. 80, 1802-1806, 1983
A:Title: beta-Hydroxyaspartic acid in vitamin K-dependent protein C.
A:Reference number: A19316; MUID:83169769; PMID:6572939
A:Contents: annotation; revision to residue 110
R:Stenflo, J.; Fernlund, P.
J. Biol. Chem. 257, 12180-12190, 1982
A:Title: Amino acid sequence of the heavy chain of bovine protein C.
A:Reference number: A18386; MUID:83007325; PMID:6896877
A:Accession: A18386
A:Molecule type: protein
A:Residues: 197-454, 'PV', <STE>
R:Esmon, N.L.; DeBault, L.E.; Esmon, C.T.
J. Biol. Chem. 258, 5548-5553, 1983
A:Title: Proteolytic formation and properties of gamma-carboxyglutamic acid-domainless F
A:Reference number: A37541; MUID:83233513; PMID:6304092
A:Contents: annotation; activation; calcium binding
R:Johnson, A.E.; Esmon, N.L.; Laue, T.M.; Esmon, C.T.
J. Biol. Chem. 258, 5554-5560, 1983
A:Title: Structural changes required for activation of protein C are induced by Ca2+ bin
A:Reference number: A37542; MUID:83233514; PMID:6406503
A:Contents: annotation; activation; calcium binding
C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that re
s.
C:Comment: Protein C is synthesized in the liver as a single chain precursor, which is c
bin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this reacti
C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stro
cognition of the thrombin-chromobomculin complex.
C:Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding
F:1-29/Domain: signal sequence (fragment) #status predicted <SIG>
F:24-83/Domain: Gla domain homology <GLA>
F:30-39/Domain: propeptide #status predicted <PRO>
F:40-194/Product: protein C light chain #status experimental <LCH>
F:98-128/Domain: EGF homology <EGH>
F:137-172/Domain: EGF homology <EG2>
F:197-456/Product: protein C heavy chain #status experimental <HCH>
F:211-210/Domain: activation peptide #status experimental <APT>
F:121-440/Domain: trypsin homology <TRY>
F:45, 46, 53, 55, 58, 59, 62, 64, 65, 68, 74/Modified site: gamma-carboxyglutamic acid (Glu) #stat
F:110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F:119-128,137-148,144-157,159-172,180-318,237-253,368-382,393-421/Disulfide bonds: #stat
F:136,289,350/Binding site: carboxylate (Asn) (covalent) #status predicted
F:252,298,397/Active site: His, Asp, Ser #status predicted
F:366/Binding site: carboxylate (Asn) (covalent) #status predicted
Query Match 58.1%; Score 115; DB 1; Length 456;
Best Local Similarity 47.6%; Pred. No. 1.6e-10;
Matches 20; Conservative 9; Mismatches 13; Indels 0; Gaps 0;
QY 1 ANSFLXXLRHSLRXRCIXXICDPFXKXIFEDVDDTLAFWS 42
DB 40 ANSFLRLPGNVERECSEVCFEAREIFONTEDTMAPWS 81
RESULT 5
EXRT
coagulation factor Xa (EC 3.4.21.6) precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Jan-1995 #sequence revision 07-Feb-1997 #text_change 08-Dec-2000
C:Accession: S49075; JC4670; P50191; P50190; I62745
R:Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.
Thromb. Res. 80, 63-73, 1995
A:Title: Evidence for competition between vitamin K-dependent clotting factors for intra
A:Reference number: A58498; MUID:96093366; PMID:8578539

A:Accession: S49075
A:Molecule type: mRNA
A:Residues: 1-482 <STAl>
A:Cross-references: EMBL:X79807; NID:G506600; PIDN:CAA56202.1; PID:G506601
A:Note: submitted to the EMBL Data Library, June 1994
A:Note: neither the complete nucleic acid sequence nor the complete translation are show
R:Stanton, C.; Ross, R.P.; Hutson, S.; Wallin, R.
Gene 169, 269-273, 1996
A:Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs.
A:Reference number: JC4670; MUID:96194815; PMID:8647460
A:Accession: JC4670
A:Molecule type: mRNA
A:Residues: 1-482 <STAl>
A:Cross-references: EMBL:X79807; NID:G506600; PIDN:CAA56202.1; PID:G506601
A:Experimental source: Cos-1 cell
R:Enyoji, K.; Miyazaki, K.; Kato, H.
J. Biochem. 109, 890-898, 1991
A:Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat plas
A:Reference number: P50190; MUID:92041742; PMID:1718949
A:Accession: P50191
A:Molecule type: protein
A:Residues: 41-58, 'X', 60-65 <ENJ1>
A:Accession: P50190
A:Molecule type: protein
A:Residues: 183-186, 'X', 188-207 <ENJ2>
R:Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Niho, Y.
Eur. J. Haematol. 52, 162-168, 1994
A:Title: Analysis of the partial nucleotide sequences and deduced primary structures of t
A:Reference number: I46196; MUID:9422160; PMID:8168596
A:Accession: I62745
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 295-383, 'G', 385-455 <MUR>
A:Cross-references: GB:D21215; NID:G415309; PIDN:BAA04756.1; PID:G455396
C:Function:
A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr
A:Pathway: blood coagulation
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutami
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-40/Domain: propeptide #status predicted <PRO>
F:25-84/Domain: Gla domain homology <GLA>
F:41-179/Product: coagulation factor X light chain #status predicted <LCH>
F:90-121/Domain: EGF homology <EG1>
F:129-164/Domain: EGF homology <EG2>
F:183-482/Product: coagulation factor X heavy chain #status predicted <HCH>
F:232-482/Product: coagulation factor Xa heavy chain #status predicted <ACT>
F:232-466/Domain: trypsin homology <TRY>
F:46, 47, 54, 56, 59, 60, 65, 66, 69, 72, 79/Modified site: gamma-carboxyglutamic acid (Glu) #stat
F:57-62, 90-101, 95-110, 112-121, 129-140, 136-149, 151-164, 172-340, 238-243, 259-275, 388-402, 41
F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F:187/Binding site: carboxylate (Asn) (covalent) #status experimental
F:208/Binding site: carboxylate (Thr) (covalent) #status predicted
F:218/Binding site: carboxylate (Asn) (covalent) #status predicted
F:231-232/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #stat
F:274,320,417/Active site: His, Asp, Ser #status predicted
Query Match 54.0%; Score 107; DB 1; Length 482;
Best Local Similarity 40.9%; Pred. No. 3.3e-09;
Matches 18; Conservative 9; Mismatches 17; Indels 0; Gaps 0;
QY 1 ANSFLXLRHSLRXRCIXXICDPFXKXIFEDVDDTLAFWSKH 44
DB 41 ANSPFEEIKGNLERECVVEICSPFEAREVEFEDNEKTEFWNKY 84
RESULT 6
EXBO
coagulation factor Xa (EC 3.4.21.6) precursor - bovine
N:Alternate names: Stuart factor
C:Species: Bos primigenius taurus (cattle)
C:Date: 24-Apr-1984 #sequence_revision 17-Mar-1987 #text_change 16-Jul-1999

C-Function:

A-Description: catalyzes the proteolytic activation of prothrombin to thrombin in the presence of factor V and fibrinogen

A-Pathway: blood coagulation

C-Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C-Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamic acid

F-1-15/Domain: signal sequence #status predicted <SIG>

F-16-40/Domain: propeptide #status predicted <PRO>

F-25-84/Domain: Gla domain homology <GUA>

F-41-180/Product: coagulation factor X light chain #status experimental <LCH>

F-90-121/Domain: EGF homology <EG1>

F-129-164/Domain: EGF homology <EG2>

F-183-492/Product: coagulation factor X heavy chain #status experimental <HCH>

F-183-233/Domain: activation peptide #status experimental <APT>

F-234-492/Product: coagulation factor Xa heavy chain #status experimental <AHC>

F-234-461/Domain: trypsin homology <TRY>

F-46-47/Domain: gamma-carboxyglutamic acid (Glu) #status predicted <GCM>

F-57-62/Domain: gamma-carboxyglutamic acid (Glu) #status predicted <GCM>

F-57-62/Domain: gamma-carboxyglutamic acid (Glu) #status predicted <GCM>

F-103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental

F-200/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental

F-208-485/Binding site: carbohydrate (Thr) (covalent) #status experimental

F-218/Binding site: carbohydrate (Asn) (covalent) #status experimental

F-233-234/Cleavage site: Arg-Ile (disulfide bonds) #status experimental

F-240-245/Domain: Arg-Ile (disulfide bonds) #status experimental

F-275-321,418/Active site: His, Asp, Ser #status predicted

Query Match 52.0%; Score 103; DB 1; Length 492;

Best Local Similarity 40.9%; Pred. No. 1.5e-08;

Matches 18; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

QY 1 ANSFLXILRHSLRXKICIXICDFXAKXIFEDVDDTLAFWSKH 44

DB 41 ANSFLEEVKQGNLEKLEACSLSEAREVFEADQTFEWSKY 84

RESULT 7

EXHU

coagulation factor Xa (EC 3.4.21.6) precursor [validated] - human

N1/Alternate names: Stuart factor

C/Species: Homo sapiens (man)

C/Date: 15-Nov-1994 #sequence revision 02-May-1994 #text change 08-Dec-2000

C/Accession: A24478; JQ0917; A24485; A25853; A22208; A21284; A20362; S59415; I54051; A000

R/Leytus, S. P.; Foster, D. C.; Kurachi, K.; Davie, E. W.

Biochemistry 25, 5098-5102, 1986

A>Title: Gene for human factor X: a blood coagulation factor whose gene organization is

A/Reference number: A24478; MUID:87028600; PMID:3768336

A/Accession: A24478

A/Molecule type: DNA

A/Residues: 1-488 <LEY>

A/Cross-references: GB:I29433; GB:M14327; NID:G459809; PIDN:AAA52764.1; PID:gi82831

R/Messier, T. L.; Pittman, D. D.; Long, G. L.; Kaufman, R. J.; Church, W. R.

Gene 99, 291-294, 1991

A>Title: Cloning and expression in COS-1 cells of a full-length cDNA encoding human coagulation factor X

A/Reference number: JQ0917; MUID:91216473; PMID:1902434

A/Accession: JQ0917

A/Molecule type: mRNA

A/Residues: 1-488 <MES>

A/Cross-references: GB:M57285; NID:G182389; PIDN:AAA52421.1; PID:G182390

R/Miao, C. H.; Leytus, S. P.; Chung, D. W.; Davie, E. W.

J. Biol. Chem. 267, 7395-7401, 1992

A>Title: Liver-specific expression of the gene coding for human factor X, a blood coagulation factor

A/Reference number: A24485; MUID:92218390; PMID:1313796

A/Accession: A24485

A/Molecule type: DNA

A/Residues: 1-15 <MIA>

A/Experimental source: liver

A/Note: sequence extracted from NCBI backbone (NCBIN:93780, NCBI:93787)

R/Kaul, R. K.; Hildebrand, B.; Roberts, S.; Jagadeeswaran, P.

Gene 41, 311-314, 1986

A>Title: Isolation and characterization of human blood-coagulation factor X cDNA.

A/Reference number: A25853; MUID:86221713; PMID:3011603

A/Accession: A25853

A/Molecule type: mRNA

A/Residues: 19-284, 'E', 289-488 <KAU>

A:Cross-references: GB:M22613; NID:gl80335; PIDN:AAA51984.1; PID:gl80336
Rifung, M.R.; Hay, C.W.; Macgillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 82, 3591-3595, 1985
A:Title: Characterization of an almost full-length cDNA coding for human blood coagulation factor X.
A:Reference number: A22208; MUID:85216545; PMID:2582420
A:Accession: A22208
A:Molecule type: mRNA
A:Residues: 13-441, 'S', 443-488 <FUN>
A:Cross-references: GB:X03194; NID:gl82840; PIDN:AAA52490.1; PID:gl82841
Riley, S.P.; Chung, D.W.; Kistiel, W.; Kurauchi, K.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 81, 3699-3702, 1984
A:Title: Characterization of a cDNA coding for human factor X.
A:Reference number: A21284; MUID:84222026; PMID:6587384
A:Accession: A21284
A:Molecule type: mRNA
A:Residues: 13-284, 'E', 289-488 <LE2>
A:Cross-references: GB:X01886
R.McMullen, B.A.; Fujikawa, K.; Sasagawa, T.; Howald, W.N.; Kwa, E.Y.; Weiss
Biochemistry 22, 2875-2884, 1983
A:Title: Complete amino acid sequence of the light chain of human blood coagulation factor X.
A:Reference number: A20362; MUID:83257207; PMID:6871157
A:Accession: A20362
A:Molecule type: protein
A:Residues: 41-179 <MCW>
R.Inoue, K.; Morita, T.
Eur. J. Biochem. 218, 153-163, 1993
A:Title: Identification of O-linked oligosaccharide chains in the activation peptides of human blood coagulation factor X.
A:Reference number: S39414; MUID:94062825; PMID:8243461
A:Accession: S39415
A:Molecule type: protein
A:Residues: 183-234 <INO>
A:Note: glycosylation sites
A:Title: Identification and characterization of beta-hydroxyaspartic acid
R.Jagadeeswaran, P.; Reddy, S.V.; Rao, K.J.; Hamsabhusanam, K.; Lyman, G.
Gene 84, 517-519, 1989
A:Title: Cloning and characterization of the 5' end (exon 1) of the gene encoding human blood coagulation factor X.
A:Reference number: I54051; MUID:90128299; PMID:2612918
A:Accession: I54051
A:Status: translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-23 <RES>
A:Cross-references: GB:M33297; NID:gl83860; PIDN:AAA52636.1; PID:q553330
R.R.Padmanabhan, K.; Padmanabhan, K.P.; Tulinsky, A.; Park, C.H.; Bode, W.; Huber, R.; Blaser, P.
J. Mol. Biol. 232, 947-966, 1993
A:Title: Structure of human factor Xa at 2.2 angstroms resolution.
A:Reference number: A49458; MUID:93360277; PMID:8355279
A:Contents: annotation; X-ray crystallography, 2.2 angstroms
A:Comment: The two chains held together by one disulfide bond are formed from a single-cysteine chain.
A:Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) or factor XIa (in the extrinsic pathway).
C:Genetics:
A:Gene: GDB:F10
A:Cross-references: GDB:119890; OMIM:227600
A:Map position: 13q34-13q34
A:Introns: 24/1; 77/3; 86/1; 124/1; 150/3; 249/3; 289/1
A:Note: Deficiency of this factor causes Stuart disease
C:Function:
A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the presence of factor V and calcium ions.
C:Subfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamic acid
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-40/Domain: propeptide #status predicted <PRO>
F:25-84/Domain: Gla domain homology <GUA>
F:41-179/Product: coagulation factor X light chain #status experimental <LCH>
F:90-121/Domain: EGF homology <EG1>
F:129-164/Domain: EGF homology <EG2>
F:183-488/Product: coagulation factor X heavy chain #status experimental <HCH>
F:183-234/Domain: activation peptide #status experimental <AP1>
F:235-488/Product: coagulation factor Xa heavy chain #status experimental <ACT>
F:235-462/Domain: trypsin homology <TRY>
F:46, 47, 54, 56, 59, 60, 65, 66, 69, 72, 79/Modified
F:57-62/Disulfide bonds: #status predicted
F:90-101, 95-110, 112-121, 129-140, 136-149, 151-164, 172-342, 241-246, 261-277, 390-404, 415-443/

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query %			DB	ID	Description
	Score	Match	Length			
1	172	86.9	461	1	PRTC_HUMAN	P04070 homo sapien
2	141	71.2	458	1	PRTC_RABIT	P02861 cryptolagus
3	133	67.2	461	1	PRTC_MOUSE	P33587 mus musculus
4	132	66.7	461	1	PRTC_RAT	P31394 rattus norv
5	126	63.6	459	1	PRTC_PIG	Q9GLP2 sus scrofa
6	115	58.1	456	1	PRTC_BOVIN	P00745 bos taurus
7	103	52.0	492	1	FA10_BOVIN	P00743 bos taurus
8	102	51.5	488	1	FA10_HUMAN	P00742 homo sapien
9	96	48.5	231	1	TMG3_HUMAN	Q9Bzd7 homo sapien
10	95	48.0	490	1	FA10_RABIT	O19045 cryptolagus
11	94	47.5	444	1	FA7_RABIT	P98139 cryptolagus
12	92	46.5	466	1	FA7_HUMAN	P08709 homo sapien
13	81	40.9	218	1	TMG1_HUMAN	O14682 homo sapien
14	78.5	39.6	617	1	THRB_RAT	P18292 rattus norv
15	78.5	39.6	618	1	THRB_MOUSE	P19221 mus musculus
16	78	39.4	226	1	TMG4_HUMAN	Q9Bzd6 homo sapien
17	78	39.4	407	1	FA7_BOVIN	P22457 bos taurus
18	77	38.9	376	1	FA10_HOPIST	P83370 holocephal
19	76	38.4	622	1	THRB_HUMAN	P00734 homo sapien
20	75	37.9	376	1	FA10_TROCA	P81428 tropidechis
21	75	37.9	475	1	FA10_CHICK	P25155 gallus galli
22	74	37.4	649	1	PRTS_YACMU	Q28520 macaca mula
23	74	37.4	676	1	PRTS_HUMAN	P07225 homo sapien
24	73	36.9	446	1	FA7_MOUSE	P70375 mus musculus
25	73	36.9	452	1	FA9_CANFA	P19540 canis famli
26	73	36.9	459	1	FA9_MOUSE	P16294 mus musculus
27	73	36.9	646	1	PRTS_RABIT	P98118 cryptolagus
28	72	36.4	675	1	PRTS_BOVIN	P07224 bos taurus
29	70	35.4	675	1	PRTS_RAT	P53813 rattus norv
30	69	34.8	461	1	FA9_HUMAN	P00740 homo sapien
31	69	34.8	461	1	FA9_PANTR	Q95nd7 pan troglod
32	66	33.3	416	1	FA9_BOVIN	P00741 bos taurus
33	65	32.8	98	1	FA10_NOTSC	P82807 notechis sc

ALIGNMENTS

RESULT 1			
ID	PTIC HUMAN	STANDARD;	PRT; 461 AA.
AC	P04070;	Q15189; Q15190;	Q16001;
DT	01-NOV-1986	(Rel. 03, Created)	
DT	01-NOV-1986	(Rel. 03, Last sequence update)	
DT	15-MAR-2004	(Rel. 43, Last annotation update)	
DE	Vitamin-K-dependent protein C precursor (EC 3.4.21.69)		
DE	(Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation factor XIV)		

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

SEQUENCE FROM N.A.
MEDLINE=85270390; PubMed=2991887;
RX

RA MEDLINS=852/0390; Fw0MEU=2991887;
RA Foster D.C., Yoshitake S., Davie E.W.;
RA "The nucleotide sequence of the gene for human protein C.";
RT Proc. Natl. Acad. Sci. U.S.A. 82:4673-4677 (1985).
RL

RP [Z] SEQUENCE FROM N.A.

RX MEDLINE=85269639; PubMed=2991859;

RA Beckmann R.J., Schmidt R.J., Santerre R.F., Plutzky J., Crabtree G.R.,
RA Long G.L.;

RT "The structure and evolution of a 461 amino acid human protein C
RT precursor and its messenger RNA, based upon the DNA sequence of
RT cloned human liver cDNAs.";

RL Nucleic Acids Res. 13:5233-5247(1985).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=86120978; PubMed=3511471;

plutzky J., Hoskins J.A., Long G.L., Crabtree G.R.;

RT "Evolution and organization of the human proteo-

Proc. Natl. Acad.
[4]

RN [4] SEQUENCE FROM N A
PP

R.F.		SEQUENCE FROM N.A.			
RA	Bieder M.T.	Carrington D.P.	Chung M.-W.	I.ee K.I.	Poe

RA KIEDEL M.O.; CALLINGTON D.F.; CHUNG M.-W.; LEE K.-L.; FOO
RA NICKERSON D.A.;

Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

RN [5]

RP SEQUENCE FROM N.A.

RC TISSUE=Colon;

RX MEDLINE=22388257; PubMed=12477932

RA Strausberg R.L., Feingold E.A., G

RA Klausner R.D., Collins F.S., Wagner

RA Altschul S.F., Zeeberg B., Buetow

RA Hopkins R.F., Jordan H., Moore T.

RA Diatchenko L., Marusina K., Farmer

RA Stapleton M., Soares M.B., Donaldson
PA Brownstein M.J., Ussidin T.B., Tosh

RA Brownstein M.J., Usdin T.B., Tosh
RA Baba S. L'Oréal N A. Peter

RA Kana S.S.; Lequellano N.A.; Pelegr
RA Bobak S.A.; McEwan P.J.; McKernan

BA Richards S.: Worley K.C.: Hale S.
KA Busak S.A.; MCEwan F.O.; McKelnam

RA Villalon D.K., Muzny D.M., Soderq

THE UNIVERSITY OF CHICAGO

RA Fahay J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Granwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [16]
RN SEQUENCE OF 106-461 FROM N.A.
RX MEDLINE=8427214; PubMed=6589623;
RA Foster D.C., Davie E.W.;
RT "Characterization of a cDNA coding for human protein C.";
RN Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984).
RN [7]
RN CARBOHYDRATE-LINKAGE SITE ASN-371.
RX MEDLINE=90293094; PubMed=1694179;
RA Miletech J.P., Broze G.J. Jr.;
RT "Beta protein C is not glycosylated at asparagine 329. The rate of
RT translation may influence the frequency of usage at asparagine-X-
RT cysteine sites.";
RL J. Biol. Chem. 265:11397-11404(1990).
RN [8]
RN HYDROXYLATION.
RX MEDLINE=92184750; PubMed=1544894;
RA Harris R.J., Ling V.T., Spellman M.W.;
RT "O-linked fucose is present in the first epidermal growth factor
RT domain of factor XII but not prorenin C.";
RL J. Biol. Chem. 267:5102-5107(1992).
RN [9]
RN 3D-STRUCTURE MODELING OF 175-450.
RX MEDLINE=94272342; PubMed=8003977;
RA Fisher C.I., Greengard J.S., Griffin J.H.;
RT "Models of the serine protease domain of the human antithrombotic
RT plasma factor activated protein C and its zymogen.";
RL Protein Sci. 3:598-599(1994).
RN [10]
RN X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 84-461.
RX MEDLINE=97157472; PubMed=9003757;
RA Mather T., Oganessyan V., Hof P., Huber R., Foundling S., Esmon C.,
RA Bode W.;
RT "The 2.8 A crystal structure of Gla-domainless activated protein C.";
RL EMBO J. 15:6822-6831(1996).
RN [11]
RN REVIEW ON PROC VARIANTS.
RX MEDLINE=93190290; PubMed=8446940;
RA Reitsma P.H., Poort S.R., Bernardi F., Gandrille S., Long G.L.,
RA Sala N., Cooper D.N.;
RT "Protein C deficiency: a database of mutations. For the Protein C & S
RT Subcommittee of the Scientific and Standardization Committee of the
RT International Society on Thrombosis and Haemostasis.";
RN Thromb. Haemost. 69:177-84(1993).
RN [12]
RN VARIANT PROC DEFICIENCY CYS-444.
RX MEDLINE=87204224; PubMed=2437584;
RA Romeo G., Hassan H.J., Staemfli S., Roncurzi L., Cianetti L.,
RA Leonardi A., Vicente V., Mannucci P.M., Bertina R.M., Peschle C.,
RA Cortese R.;
RT "Hereditary thrombophilia: identification of nonsense and missense
RT mutations in the protein C gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:2829-2832(1987).
RN [13]
RN VARIANT PROC DEFICIENCY TRP-211.
RX MEDLINE=90098906; PubMed=2602169;
RA Grundy C.B., Chitcolle A., Talbot S., Bevan D., Kakkar V.V.,
RA Cooper D.N.;
RT "Protein C London 1: recurrent mutation at Arg-169 (GGG-->TGG) in
RT the protein C gene causing thrombosis.";
RL Nucleic Acids Res. 17:10513-10513(1989).
RN [14]
RN VARIANT PROC DEFICIENCY CYS-272.
RX MEDLINE=91329836; PubMed=1868249;
RA Reitsma P.H., Poort S.R., Allaart C.F., Briet E., Bertina R.M.;
RT "The spectrum of genetic defects in a panel of 40 Dutch families with
RT symptomatic protein C deficiency type I: heterogeneity and founder
RT effects.";
RL Blood 78:890-894(1991).
RN [15]
RN VARIANTS PROC DEFICIENCY ALA-62 AND MET-76.
RX MEDLINE=92190481; PubMed=1347706;
RA Bovill E.G., Tomczak J.A., Grant B., Bhushan F., Pillemer E.,
RA Rainville I.R., Long G.L.;
RT "Protein C Vermont: symptomatic type II protein C deficiency
RT associated with two GLA domain mutations.";
RL Blood 79:1456-1465(1992).
RN [16]
RN VARIANT PROC DEFICIENCY ASP-418.
RX MEDLINE=92305321; PubMed=1611081;
RA Suganahara Y., Miura O., Yuen P., Aoki N.;
RT "Protein C deficiency Hong Kong 1 and 2: hereditary protein C
RT deficiency caused by two mutant alleles, a 5-nucleotide deletion and
RT a missense mutation.";
RL Blood 80:126-133(1992).
RN [17]
RN VARIANT PROC DEFICIENCY LEU-289.
RX MEDLINE=92380860; PubMed=1511988;
RA Grundy C.B., Chisholm M., Kakkar V.V., Cooper D.N.;
RT "A novel homozygous missense mutation in the protein C (PROC) gene
RT causing recurrent venous thrombosis.";
RL Hum. Genet. 89:683-684(1992).
RN [18]
RN VARIANTS PROC DEFICIENCY GLN-220 AND TRP-220.
RX MEDLINE=92380861; PubMed=1511989;
RA Grundy C.B., Schulman S., Tengborn L., Kakkar V.V., Cooper D.N.;
RT "Two different missense mutations at Arg 178 of the protein C (PROC)
RT gene causing recurrent venous thrombosis.";
RL Hum. Genet. 89:685-686(1992).
RN [19]
RN VARIANT PROC DEFICIENCY GLN-220.
RX MEDLINE=93250852; PubMed=1301959;
RA Gandrille S., Vidaud M., Alach M., Alhenc-Gelas M., Fischer A.M.,
RA Gouault-Heilman M., Toulon P., Flessinger J.N., Goossens M.;
RT "Two novel mutations responsible for hereditary type I protein C
RT deficiency: characterization by denaturing gradient gel
RT electrophoresis.";
RL Hum. Mutat. 1:491-500(1992).
RN [20]
RN VARIANT PROC DEFICIENCY SER-334.
RX MEDLINE=92276939; PubMed=1593215;
RA Yamamoto K., Matsushita T., Sugiyama I., Takamatsu J., Iwasaki E.,
RA Wada H., Deguchi K., Shirakawa S., Saito H.;
RT "Homozygous protein C deficiency: identification of a novel missense
RT mutation that causes impaired secretion of the mutant protein C.";
RL J. Lab. Clin. Med. 119:682-689(1992).
RN [21]
RN VARIANTS PROC DEFICIENCY TRP-38; CYS-42; HIS-42; GLN-271 AND ASN-294.
RX MEDLINE=93313192; PubMed=8324221;
RA Gandrille S., Alhenc-Gelas M., Gaussem P., Aillaud M.-F., Dupuy E.,
RA Juhan-Vague I., Riach M.;
RT "Five novel mutations located in exons III and IX of the protein C
RT gene in patients presenting with defective protein C anticoagulant
RT activity.";
RL Blood 82:159-168(1993).
RN [22]
RN VARIANTS PROC DEFICIENCY GLY-14; GLN-211; TYR-244; GLN-253; LEU-321;
CYS-328; ILE-385; THR-388 AND VAL-388.
RX MEDLINE=93271391; PubMed=8499565;
RA Poort S.R., Pabinger-Fasching I., Mannhalter C., Reitsma P.H.,
RA Bertina R.M.;
RT "Twelve novel and two recurrent mutations in 14 Austrian families
RT with hereditary protein C deficiency.";
RL Blood Coagul. Fibrinolysis 4:273-280(1993).
RN [23]
RN VARIANT PROC DEFICIENCY TRP-57.
RX MEDLINE=93271396; PubMed=8499568;


```

FT DISULFID 396 424 BY SIMILARITY
FT CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 459 AA; 51866 MW; 8541AAC14CC16D09 CRC64;

Query Match 63.6%; Score 126; DB 1; Length 459;
Best Local Similarity 54.5%; Pred. No. 2,9e-13;
Matches 24; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

QY 1 ANSFLXLLHSSILRXICIXXICDFAKXKXIFEDVDVDTLAFWSKH 44
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 42 ANSFLLELPSPSLERCKEETCDFEAREBIFONTENTAFWSKY 85

RESULT 6
PRTC_BOVIN STANDARD; PRT; 456 AA.
ID PRTC_BOVIN
AC P00745;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Vitamin-K-dependent protein C precursor (EC 3.4.21.69)
DE (Autoproteolysin IIa) (Anticoagulant protein C) (Blood coagulation
DE factor XIV) (Fragment).
GN PROC.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_Taxid:9913;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=85014826; PubMed=6091100;
RA Long G.L., Balagaje R.M., McGillivray R.T.A.;
RT "Cloning and sequencing of liver cDNA coding for bovine protein C.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5653-5656(1984).
RN [2]
RX SEQUENCE OF 40-194, AND CARBOHYDRATE-LINKAGE SITE ASN-136.
RA MEDLINE=83007325; PubMed=6896876;
RA Fernlund P., Stenflo J.;
RT "Amino acid sequence of the light chain of bovine protein C.";
RN [3]
RX J. Biol. Chem. 257:12170-12179(1982).
RN [4]
RX REVISION TO 110.
RX MEDLINE=83169769; PubMed=6572939;
RA Drakenberg T., Fernlund P., Roepstorff P., Stenflo J.;
RT "Beta-hydroxyaspartic acid in vitamin K-dependent protein C.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:1802-1806(1983).
RN [5]
RX SEQUENCE OF 197-456, AND CARBOHYDRATE-LINKAGE SITES ASN-289; ASN-350
RX AND ASN-366.
RX MEDLINE=83007326; PubMed=6896877;
RA Stenflo J., Fernlund P.;
RT "Amino acid sequence of the heavy chain of bovine protein C.";
RN [6]
RX J. Biol. Chem. 257:12180-12190(1982).
RN [7]
RX PROCESSING, AND CALCIUM-BINDING DATA.
RX MEDLINE=83213513; PubMed=6304092;
RA Esmon N.L., Debault L.E., Esmon C.T.;
RT "Proteolytic formation and properties of gamma-carboxyglutamic acid-
RT domainless protein C.";
RN [8]
RX J. Biol. Chem. 258:5548-5553(1983).
RN [9]
RX PROCESSING, AND CALCIUM-BINDING DATA.
RX MEDLINE=83213514; PubMed=6406503;
RA Johnson A.B., Esmon N.L., Laue T.M., Esmon C.T.;
RT "Structural changes required for activation of protein C are induced
RT by Ca2+ binding to a high affinity site that does not contain gamma-
RT carboxyglutamic acid.";
RN [10]
RX J. Biol. Chem. 258:5554-5560(1983).
CC -!- FUNCTION: Protein C is a vitamin K-dependent serine protease that
    regulates blood coagulation by inactivating factors Va and VIIIa

```

```

CC in the presence of calcium ions and phospholipids.
CC -!- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIIa.
CC -!- SUBUNIT: Synthesized as a single chain precursor, which is cleaved
CC into a light chain and a heavy chain held together by a disulfide
CC bond. The enzyme is then activated by thrombin, which cleaves a
CC tetradecapeptide from the amino end of the heavy chain; this is
CC reaction, which occurs at the surface of endothelial cells, is
CC strongly promoted by thrombomodulin.
CC -!- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
CC -!- PM: The vitamin K-dependent, enzymatic carboxylation of some Glu
CC residues allows the modified protein to bind calcium.
CC -!- MISCELLANEOUS: Calcium also binds, with stronger affinity to
CC another site, beyond the GLA domain. This GLA-independent binding
CC site is necessary for the recognition of the thrombin-
CC thrombomodulin complex.
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- SIMILARITY: Contains 2 EGF-like domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: K02435; AAA30685.1; -.
CC PIR: A26250; KXBO.
CC HSSP: P04070; IPCU.
CC MEROPS: S01.218; -.
CC -----
CC InterPro: IPR000152; Asx_hydroxyl_S.
CC InterPro: IPR009003; Cys_Ser_trypsin.
CC InterPro: IPR001881; EGF_Ca.
CC InterPro: IPR006209; EGF_like.
CC InterPro: IPR002383; GLA_blood.
CC InterPro: IPR006210; IEGF.
CC InterPro: IPR001254; Peptidase_S1.
CC InterPro: IPR001314; Peptidase_S1A.
CC InterPro: IPR000294; VitK_dep_GLA.
CC Pfam: PF00008; EGF_2.
CC Pfam: PF00594; gla_1.
CC Pfam: PF00089; crypsin; 1.
CC PRINTS: PR00722; CHYMOTRYPSIN.
CC PRINTS: PR00001; GLABLOOD.
CC SMART: SM00181; EGF_2.
CC SMART: SM00069; EGF_1.
CC SMART: SM00020; TRYD_SPC_1.
CC PROSITE: PS00010; ASX_HYDROXYL; 1.
CC PROSITE: PS00022; EGF_1; 1.
CC PROSITE: PS01186; EGF_2; 2.
CC PROSITE: PS00026; EGF_3; 1.
CC PROSITE: PS01187; EGF_CA; 1.
CC PROSITE: PS00011; GLU_CARBOXYLATION; 1.
CC PROSITE: PS00240; TRYPSIN_DOM; 1.
CC PROSITE: PS00134; TRYPSIN_HIS; 1.
CC PROSITE: PS00135; TRYPSIN_SER; 1.
CC Blood coagulation; Glycoprotein; Serine protease;
CC Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
CC EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
CC NON_TER 1 1
CC SIGNAL <1 29
CC PROPEP 30 39
CC CHAIN 40 194
CC CHAIN 197 456
CC PEPTIDE 197 210
CC DOMAIN 94 129
CC DOMAIN 133 173
CC DOMAIN 211 456
CC MOD_RES 45 45
CC MOD_RES 46 46
CC MOD_RES 53 53
CC MOD_RES 55 55
CC PROTEIN C LIGHT CHAIN.
CC PROTEIN C HEAVY CHAIN.
CC ACTIVATION PEPTIDE.
CC EGF-LIKE 1.
CC EGF-LIKE 2.
CC SERINE PROTEASE.
CC GAMMA-CARBOXYGLUTAMIC ACID.
CC GAMMA-CARBOXYGLUTAMIC ACID.
CC GAMMA-CARBOXYGLUTAMIC ACID.

```


like domain in coagulation factor X.";
 [13] J. Biol. Chem. 267:19642-19649(1992).
 RP STRUCTURE BY NMR OF 41-126.
 RX MEDLINE=96387194; PubMed=8794734;
 RA Sunnerhagen M., Olah G.A., Stenflo J., Forsen S., Drakenberg T.,
 RA Trewthella J.;
 RT "The relative orientation of Gla and EGF domains in coagulation
 RT factor X is altered by Ca²⁺ binding to the first EGF domain. A
 RT combined NMR-small angle X-ray scattering study.";
 RL Biochemistry 35:11547-11559(1996).
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
 CC converts prothrombin to thrombin in the presence of factor Va,
 CC calcium and phospholipid during blood clotting.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
 CC Arg-|-Ile bonds in prothrombin to form thrombin.
 CC -1- SUBUNIT: The two chains are formed from a single-chain precursor
 CC by the excision of two Arg residues and are held together by 1 or
 CC more disulfide bonds.
 CC -1- PTM: The vitamin K-dependent, enzymatic carboxylation of some
 CC glutamate residues allows the modified protein to bind calcium.
 CC -1- PTM: N- and O-glycosylated.
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
 CC -1- MISCELLANEOUS: Calcium also binds, with stronger affinity to
 CC another site, beyond the Gla domain.
 CC -1- SIMILARITY: Belongs to peptidase family S1.
 CC -1- SIMILARITY: Contains 2 EGF-like domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X00673; CAA25286.1; --
 DR PIR; A22867; EXBO.
 DR PDB; IAFQ; 31-JAN-94.
 DR PDB; ICCF; 31-MAY-94.
 DR PDB; IWHF; 15-MAY-97.
 DR PDB; IWHF; 15-MAY-97.
 DR PDB; IIOB; 21-JAN-03.
 DR PDB; IKIG; 28-OCT-98.
 DR MEROPS; S01.216; --
 DR GlycoSuiteDB; F00743; --
 DR InterPro; IPR000152; Asx_hydroxyl_S.
 DR InterPro; IPR009003; Cys_Ser_trypsin.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00594; Gla; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS00026; EGF_3; 1.
 DR PROSITE; PS01197; EGF_CA; 1.
 DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
 DR PROSITE; PS0240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.

KW Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;
 KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
 KW Signal; Zymogen; EGF-like domain; Repeat; Sulfation; 3D-structure.
 FT SIGNAL 1 23
 FT PROPEP 24 40
 FT CHAIN 41 180
 FT CHAIN 183 492
 FT PROPEP 183 233
 FT CHAIN 234 492
 FT CHAIN 234 492
 FT PROPEP 476 492
 FT DOMAIN 86 122
 FT DOMAIN 125 165
 FT DOMAIN 234 492
 FT ACT_SITE 275 275
 FT ACT_SITE 321 321
 FT ACT_SITE 418 418
 FT MOD_RES 46 46
 FT MOD_RES 47 47
 FT MOD_RES 54 54
 FT MOD_RES 56 56
 FT MOD_RES 59 59
 FT MOD_RES 60 60
 Query Match 52.0%; Score 103; DB 1; Length 492;
 Best Local Similarity 40.9%; Pred. No. 2.3e-03;
 Matches 18; Conservative 8; Mismatches 18; Indels 0; Gaps 0;
 QY 1 ANSLFXLRHSSLRXCIXXICDPFXKXIFEDVDDTLAFLSKH 44
 DB 41 ANSPLEVKQGNLERCEAECSLEAREVFEDREQIDEFWSKY 84
 RESULT 8
 FA10 HUMAN STANDARD; PRT; 488 AA.
 ID FA10 HUMAN STANDARD; PRT; 488 AA.
 AC P00742; O14340;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
 GN F10.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91216473; PubMed=1902434;
 RA Messier T.L., Pittman D.D., Long G.L., Kaufman R.J., Church W.R.;
 RT "Cloning and expression in COS-1 cells of a full-length cDNA encoding
 RT human coagulation factor X.";
 RL Gene 99:291-294(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87026600; PubMed=3768336;
 RA Leytus S.P., Foster D.C., Kurachi K., Davie E.W.;
 RT "Gene for human factor X: a blood coagulation factor whose gene
 RT organization is essentially identical with that of factor IX and
 RT protein C.";
 RL Biochemistry 25:5098-5102(1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Rieder M.J., Armel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
 RA Ozuna M., Peel C.L., Toth E.J., Yi Q., Nickerson D.A.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gurnatne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[5]
SEQUENCE OF 13-488 FROM N.A.
RX MEDLINE=85216545; PubMed=2582420;
RA Fung M.R., Hay C.W., McGillivray R.T.A.;
RT "Characterization of an almost full-length cDNA coding for human
RT blood coagulation factor X";
Proc. Natl. Acad. Sci. U.S.A. 82:3591-3595(1985).
[6]
SEQUENCE OF 19-488 FROM N.A.
RX TISSUE=Liver;
RC MEDLINE=86221713; PubMed=3011603;
RA Kaul R.K., Hildebrand B., Roberts S., Jagadeeswaran P.;
RT "Isolation and characterization of human blood-coagulation factor X
RT cDNA";
Gene 41:311-314(1986).
[7]
SEQUENCE OF 41-179.
RX MEDLINE=83257207; PubMed=6871167;
RA McMullen B.A., Fujikawa K., Kiesel W., Sasagawa T., Howald W.N.,
RA Kwa E.Y., Weinstein B.;
RT "Complete amino acid sequence of the light chain of human blood
RT coagulation factor X: evidence for identification of residue 63 as
RT beta-hydroxyaspartic acid";
Biochemistry 22:2875-2884(1983).
[8]
SEQUENCE OF 115-488 FROM N.A., AND TISSUE SPECIFICITY.
RC TISSUE=Liver;
RX MEDLINE=84222026; PubMed=6587384;
RA Leytus S.P., Chung D.W., Kiesel W., Kurachi K., Davie E.W.;
RT "Characterization of a cDNA coding for human factor X";
Proc. Natl. Acad. Sci. U.S.A. 81:3699-3702(1984).
[9]
SEQUENCE OF 183-234, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=94062825; PubMed=8243461;
RA Inoue K., Morita T.;
RT "Identification of O-linked oligosaccharide chains in the activation
RT peptides of blood coagulation factor X: the role of the carbohydrate
RT moieties in the activation of factor X";
Eur. J. Biochem. 218:153-163(1993).
[10]
SEQUENCE OF 1-23 FROM N.A.
RX MEDLINE=90128299; PubMed=2612918;
RA Jagadeeswaran P., Reddy S.V., Rao K.J., Hamsabhusanam K., Lyman G.;
RT "Cloning and characterization of the 5' end (exon 1) of the gene
RT encoding human factor X";
Gene 84:517-519(1989).
[11]
X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 86-179 AND 235-278.
RX MEDLINE=93360277; PubMed=835279;
RA Padmanabhan K., Padmanabhan K.P., Tulinsky A., Park C.H., Bode W.,
RA Huber R., Blankenship D.T., Cardin A.D., Kiesel W.;
RT "Structure of human des(1-45) factor Xa at 2.2-A resolution";
J. Mol. Biol. 232:947-966(1993).
[12]
X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.
RX MEDLINE=98283982; PubMed=9618463;

Kamata K., Kawamoto H., Honma T., Iwama T., Kim S.H.;
RT "Structural basis for chemical inhibition of human blood coagulation
RT factor Xa";
Proc. Natl. Acad. Sci. U.S.A. 95:6630-6635(1998).
[13]
VARIANT'S ILE-7 AND HIS-30.
RX MEDLINE=99318093; PubMed=10391209;
RA Cargill M., Altschuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
RA Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,
RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.G.,
RA Lander E.S.;
RT "Characterization of single-nucleotide polymorphisms in coding regions
RT of human genes";
Nat. Genet. 22:231-238(1999).
[14]
ERRATUM.
RA Cargill M., Altschuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
RA Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,
RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.G.,
RA Lander E.S.;
RT "FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
RT converts prothrombin to thrombin in the presence of factor Va,
RT calcium and phospholipid during blood clotting."
CC CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
CC Arg-|-Ile bonds in prothrombin to form thrombin.
CC SUBUNIT: The two chains are formed from a single-chain precursor
CC by the excision of two Arg residues and are held together by 1 or
CC more disulfide bonds.
CC TISSUE SPECIFICITY: Plasma; synthesized in the liver.
CC PTM: The vitamin K-dependent, enzymatic carboxylation of some
CC glutamate residues allows the modified protein to bind calcium.
CC PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
CC SIMILARITY: Belongs to peptidase family S1.
CC SIMILARITY: Contains 2 EGF-like domains.

THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

EMBL; K03194; AAA52490.1; -
EMBL; M57285; AAA52421.1; -
EMBL; AF503510; AAM19347.1; -
EMBL; BC046125; AAH46125.1; -
EMBL; L29433; AAA52764.1; -
EMBL; L00390; AAA52764.1; JOINED.
EMBL; L00391; AAA52764.1; JOINED.
EMBL; L00392; AAA52764.1; JOINED.
EMBL; L00393; AAA52764.1; JOINED.
EMBL; L00394; AAA52764.1; JOINED.
EMBL; L00395; AAA52764.1; JOINED.
EMBL; L00396; AAA52764.1; JOINED.
EMBL; M22613; AAA51984.1; -
EMBL; K01886; AAA52486.1; -
EMBL; M33297; AAA52636.1; -
PIR; A24478; EXHU.
PDB; 1HCG; 08-MAY-95.
PDB; 1FAX; 29-OCT-97.
PDB; 1FXV; 17-JUN-98.
PDB; 1XKA; 23-MAR-99.
PDB; 1XKB; 23-MAR-99.
PDB; 1EZQ; 20-SEP-00.
PDB; 1FOR; 20-SEP-00.
PDB; 1FOS; 20-SEP-00.
PDB; 1FJS; 17-NOV-00.
PDB; 1G2L; 20-OCT-01.
PDB; 1G2M; 20-OCT-01.


```
DR PDB; 1KSN; 19-JUN-02.
DR PDB; 1KYE; 11-FEB-03.
DR PDB; 1MQ5; 28-JAN-03.
DR PDB; 1MQ6; 28-JAN-03.
DR PDB; 1NFU; 28-JAN-03.
DR PDB; 1NFW; 25-FEB-03.
DR PDB; 1NFX; 25-FEB-03.
DR PDB; 1NFY; 25-FEB-03.
DR MEROPS; S01.216; -.
DR GlycoSuiteDB; P00742; -.
DR Genew; HGNC:3528; F10.
DR MIM; 134530; -.
DR MIM; 227600; -.
DR GO; GO:0005576; C:extracellular; TAS.
DR GO; GO:0003804; F:blood coagulation factor X activity; TAS.
DR GO; GO:0007596; P:blood coagulation; TAS.

Query Match 51.5%; Score 102; DB 1; Length 488;
Best Local Similarity 40.94; Pred. No. 3.3e-09;
Matches 18; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

QY 1 ANSFLXLRHSSLRXCIXXICDFXAXKXIFEDVDDTLAFWSKH 44
    ||||| : : : : : : : : : : : : : : : : : :
DB 41 ANSFLXLRHSSLRXCIXXICDFXAXKXIFEDVDDTLAFWSKH 44
    ||||| : : : : : : : : : : : : : : : : : :

RESULT 9
TMG3 HUMAN
ID -TMG3 HUMAN STANDARD; PRT; 231 AA.
AC Q9BZD7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Transmembrane gamma-carboxyglutamic acid protein 3 precursor.
GN TMG3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spinal cord;
RX MEDLINE=21117044; PubMed=11171957;
RA Kulman J.D., Harris J.E., Xie L., Davie E.W.;
RT "Identification of two novel transmembrane gamma-carboxyglutamic acid
  proteins expressed broadly in fetal and adult tissues.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:1370-1375(2001).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in brain, lung, kidney and heart.
CC -!- PTM: Gla residues are produced after subsequent posttranslational
  modifications of glutamate by a vitamin K-dependent gamma-
  carboxylase.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
  the European Bioinformatics Institute. There are no restrictions on its
  use by non-profit institutions as long as its content is in no way
  CC modified and this statement is not removed. Usage by and for commercial
  entities requires a license agreement (See http://www.isb-sib.ch/announce/
  or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF326350; AAK00955.1; -.
CC HSSP; P00740; 1CFH.
CC GO; GO:0016021; C:integral to membrane; NAS.
CC InterPro; IPR002383; GLA_blood.
CC InterPro; IPR000294; VitK_dep_GLA.
CC Pfam; P00594; gla_1.
CC PRINTS; P00001; GLABLOOD.
CC SMART; SM00069; GLA; 1.
CC PROSITE; PS00111; GLU CARBOXYLATION; 1.
CC Gamma-carboxyglutamic acid; Vitamin K; Transmembrane.
CC PROPEP 1 19 POTENTIAL.
CC CHAIN 20 231 TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
  FT

PDB; 1KSN; 19-JUN-02.
PDB; 1KYE; 11-FEB-03.
PDB; 1MQ5; 28-JAN-03.
PDB; 1MQ6; 28-JAN-03.
PDB; 1NFU; 28-JAN-03.
PDB; 1NFW; 25-FEB-03.
PDB; 1NFX; 25-FEB-03.
PDB; 1NFY; 25-FEB-03.
MEROPS; S01.216; -.
GlycoSuiteDB; P00742; -.
Genew; HGNC:3528; F10.
MIM; 134530; -.
MIM; 227600; -.
GO; GO:0005576; C:extracellular; TAS.
GO; GO:0003804; F:blood coagulation factor X activity; TAS.
GO; GO:0007596; P:blood coagulation; TAS.

Query Match 48.5%; Score 96; DB 1; Length 231;
Best Local Similarity 39.0%; Pred. No. 1.4e-08;
Matches 16; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 1 ANSFLXLRHSSLRXCIXXICDFXAXKXIFEDVDDTLAFW 41
    ||||| : : : : : : : : : : : : : : : : : :
DB 20 ANEFLLELRQGTIERECMEECISYEVEKVFENKKTMEFW 60
    ||||| : : : : : : : : : : : : : : : : : :

RESULT 10
FA10 RABBIT
ID FA10 RABBIT STANDARD; PRT; 490 AA.
AC O19045;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
GN F10.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97256311; PubMed=9101642;
RA Pendurthi U.R., Anderson K.D., James H.L.;
RT "Characterization of a full-length cDNA for rabbit factor X.";
RL Thromb. Res. 85:503-514(1997).
CC -!- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
  converts prothrombin to thrombin in the presence of factor Va,
  calcium and phospholipid during blood clotting.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
  Arg-|-Ile bonds in prothrombin to form thrombin.
CC -!- SUBUNIT: The two chains are formed from a single-chain precursor
  by the excision of two Arg residues and are held together by 1 or
  more disulfide bonds.
CC -!- PTM: The vitamin K-dependent, enzymatic carboxylation of some
  CC glutamate residues allows the modified protein to bind calcium (By
  similarity).
CC -!- PTM: N- and O-glycosylated (By similarity).
CC -!- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
  CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY)
  CC (BY SIMILARITY).
CC -!- MISCELLANEOUS: Calcium also binds, with stronger affinity to
  CC another site, beyond the GLA domain.
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- SIMILARITY: Contains 2 EGF-like domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
  the European Bioinformatics Institute. There are no restrictions on its
  use by non-profit institutions as long as its content is in no way
  CC modified and this statement is not removed. Usage by and for commercial
  entities requires a license agreement (See http://www.isb-sib.ch/announce/
  or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF003200; AAB62542.1; -.
CC HSSP; P00742; IHCG.
CC MEROPS; S01.216; -.
CC InterPro; IPR000152; Asx_hydroxyl_S.
CC InterPro; IPR009003; Cys_Ser_trypsin.
CC InterPro; IPR000742; EGF_2.
CC InterPro; IPR001881; EGF_Ca.
CC InterPro; IPR001438; EGF_II.
CC InterPro; IPR006209; EGF-like.
CC InterPro; IPR002383; GLA_blood.
```

InterPro; IPR001254; Peptidase S1.
 InterPro; IPR001314; Peptidase S1A.
 Pfam; PF000294; VitK_dep_GLA.
 Pfam; PF00008; EGF; 2.
 Pfam; PF00594; gla; 1.
 PRINTS; PR00089; trypsin; 1.
 PRINTS; PR00722; CHYMOTRYPSIN.
 PRINTS; PR00010; EGF_BLOOD.
 PRINTS; PR00001; GLABLOOD.
 SMART; SM00179; EGF_CA; 1.
 SMART; SM00069; GLA; 1.
 SMART; SM00020; TRYP_SPC; 1.
 PROSITE; PS00010; ASX_HYDROXYL; 1.
 PROSITE; PS00022; EGF_1; 1.
 PROSITE; PS01186; EGF_2; 2.
 PROSITE; PS00026; EGF_3; 1.
 PROSITE; PS01187; EGF_CA; 1.
 PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 PROSITE; PS00240; TRYPSIN_DOM; 1.
 PROSITE; PS00134; TRYPSIN_HIS; 1.
 PROSITE; PS00135; TRYPSIN_SER; 1.
 Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;
 gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
 Signal; Zymogen; EGF-like domain; Repeat.
 SIGNAL 1 20 POTENTIAL.
 PROPEP 21 40 BY SIMILARITY.
 CHAIN 41 180 FACTOR X LIGHT CHAIN.
 CHAIN 184 490 FACTOR X HEAVY CHAIN.
 PROPEP 184 232 ACTIVATION PEPTIDE.
 CHAIN 233 490 ACTIVATED FACTOR XA, HEAVY CHAIN.
 DOMAIN 86 122 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
 DOMAIN 125 165 EGF-LIKE 2.
 DOMAIN 233 490 SERINE PROTEASE.
 MOD_RES 46 46 GAMMA-CARBOXYGLUTAMIC ACID (BY
 MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID (BY
 MOD_RES 54 54 GAMMA-CARBOXYGLUTAMIC ACID (BY
 MOD_RES 56 56 GAMMA-CARBOXYGLUTAMIC ACID (BY
 MOD_RES 59 59 GAMMA-CARBOXYGLUTAMIC ACID (BY
 MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID (BY
 MOD_RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID (BY
 MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID (BY
 MOD_RES 69 69 GAMMA-CARBOXYGLUTAMIC ACID (BY
 MOD_RES 72 72 GAMMA-CARBOXYGLUTAMIC ACID (BY
 MOD_RES 75 75 GAMMA-CARBOXYGLUTAMIC ACID (BY
 MOD_RES 79 79 GAMMA-CARBOXYGLUTAMIC ACID (BY
 MOD_RES 103 103 HYDROXYLATION (BY SIMILARITY).
 ACT_SITE 274 274 CHARGE RELAY SYSTEM.
 ACT_SITE 320 320 CHARGE RELAY SYSTEM.
 ACT_SITE 417 417 CHARGE RELAY SYSTEM.
 DISULFID 90 101 BY SIMILARITY.
 DISULFID 95 110 BY SIMILARITY.
 DISULFID 112 121 BY SIMILARITY.
 DISULFID 129 140 BY SIMILARITY.
 DISULFID 136 149 BY SIMILARITY.
 DISULFID 151 164 BY SIMILARITY.
 DISULFID 172 340 INTERCHAIN (BY SIMILARITY).
 DISULFID 239 244 BY SIMILARITY.
 DISULFID 259 275 BY SIMILARITY.
 DISULFID 388 402 BY SIMILARITY.
 DISULFID 413 441 BY SIMILARITY.
 CARBOHYD 61 61 N-LINKED (GLCNAC...) (POTENTIAL).

FT CARBOHYD 187 187 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 205 205 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 490 AA; 53965 MW; 3A39FA85AF2A6D11 CRC64;
 Query Match 48.0%; Score 95; DB 1; Length 490;
 Best Local Similarity 40.9%; Pred No. 4.9e-08;
 Matches 18; Conservative 8; Mismatches 18; Indels 0; Gaps 0;
 QY 1 ANSFLXLRHSSLRXCIXXICDFXAXXIFEDVDDTLAFWSKH 44
 DB 41 ANSFLEELKGNLERECMEENCSEVEALEVEDREKTNFNNKY 84
 RESULT 11
 ID FA7_RABIT STANDARD; PRT; 444 AA.
 AC P98139; P79224;
 DT 01-FEB-1996 (Rel. 33; Created)
 DT 15-JUL-1998 (Rel. 36; Last sequence update)
 DE 10-OCT-2003 (Rel. 42; Last annotation update)
 DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
 conversion accelerator).
 GN F7.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=93190306; PubMed=8383365;
 RA Brothers A.B., Clarke B.J., Sheffield W.P., Blajchman M.A.;
 RT "Complete nucleotide sequence of the cDNA encoding rabbit coagulation
 factor VII.";
 RL Thromb. Res. Suppl. 69:231-238(1993).
 RN [2]
 RP REVISION TO 395.
 RC TISSUE=Liver;
 RA Ruiz S.R., Blajchman M.A., Clarke B.J.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Circulates in the blood in a zymogen form. Factor VII is
 converted to factor VIIa by factor Xa, factor XIIa, factor IXa, or
 thrombin by minor proteolysis. In the presence of tissue factor
 and calcium ions, factor VIIa then converts factor X to factor Xa
 by limited proteolysis. Factor VIIa will also convert factor IX to
 factor IXa in the presence of tissue factor and calcium (By
 similarity).
 CC -!- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
 form factor Xa.
 CC -!- SUBUNIT: Heterodimer of a light chain and a heavy chain linked by
 a disulfide bond (By similarity).
 CC -!- TISSUE SPECIFICITY: Plasma.
 CC -!- PTM: The vitamin K-dependent, enzymatic carboxylation of some
 glutamate residues allows the modified protein to bind calcium (By
 similarity).
 CC -!- SIMILARITY: Belongs to peptidase family S1.
 CC -!- SIMILARITY: Contains 2 EGF-like domains.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC EMBL; U77477; AAB37326.1; -.
 DR HSSP; P08709; 1FAK.
 DR MEROPS; S01.215; -.
 DR InterPro; IPR000152; Asx_hydroxyl_S.
 DR InterPro; IPR009003; Cys_ser_trypsin.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.

RT first EGF-like domain of clotting factors VII and IX and protein Z.";
 RL Adv. Exp. Med. Biol. 281:121-131(1990).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
 RX MEDLINE=96175641; PubMed=8598903;
 RA Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,
 RA Konigsberg W.H., Nemerson Y., Kirchhofer D.;
 RT "The crystal structure of the complex of blood coagulation factor
 RT VIIa with soluble tissue factor.";
 RL Nature 380:41-46(1996).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
 RX MEDLINE=99126538; PubMed=9925787;
 RA Zhang E., St Charles R., Tulinsky A.;
 RT "Structure of extracellular tissue factor complexed with factor VIIa
 RT inhibited with a BPR1 mutant.";
 RL J. Mol. Biol. 285:2089-2104(1999).
 RN [10]
 RP STRUCTURE BY NMR OF 105-145.
 RX MEDLINE=98367502; PubMed=9692950;
 RA Muranyi A., Finn B.E., Gippert G.P., Forsen S., Stenflo J.,
 RA Drakenberg T.;
 RT "Solution structure of the N-terminal EGF-like domain from human
 RT factor VII.";
 RL Biochemistry 37:10605-10615(1998).
 RN [11]
 RP VARIANT GLN-364.
 RX MEDLINE=91300046; PubMed=2070047;
 RA O'Brien D.P., Gale K.M., Anderson J.S., McVey J.H., Miller G.J.,
 RA Meade T.W., Tuddenham E.G.D.;
 RT "Purification and characterization of factor VII 304-Gln: a variant
 RT molecule with reduced activity isolated from a clinically unaffected
 RT male.";
 RL Blood 78:132-140(1991).
 RN [12]
 RP VARIANTS GLN-364 AND PHE-370.
 RX MEDLINE=92340074; PubMed=1634227;
 RA Marchetti G., Patrachini P., Gemmati D., Derosa V., Pinotti M.,
 RA Rodrigo G., Casonato A., Girolami A., Bernardi F.;
 RT "Detection of two missense mutations and characterization of a repeat
 RT polymorphism in the factor VII gene (F7).";
 RL Hum. Genet. 89:497-502(1992).
 RN [13]
 RP VARIANT TVR-238.
 RX MEDLINE=93372811; PubMed=8364544;
 RA Marchetti G., Ferrati M., Patrachini P., Redaelli R., Bernardi F.;
 RT "A missense mutation (178Cys-->Tyr) and two neutral dimorphisms
 RT (115His and 333Ser) in the human coagulation factor VII gene.";
 RL Hum. Mol. Genet. 2:1055-1056(1993).
 RN [14]
 RP VARIANTS.
 RX MEDLINE=94061028; PubMed=8242057;
 RA Takamiya O., Xenball-Cook G., Martin D.M.A., Cooper D.N.,
 RA von Felten A., Meili E., Hahn I., Prangnell D.R., Lumley H.,
 RA Tuddenham E.G.D., McVey J.H.;
 RT "Detection of missense mutations by single-strand conformational
 RT polymorphism (SSCP) analysis in five dysfunctional variants of
 RT coagulation factor VII.";
 RL Hum. Mol. Genet. 2:1355-1359(1993).
 RN [15]
 RP VARIANTS CHARLOTTE GLN-139 AND GLN-212.
 RX MEDLINE=94264305; PubMed=8204879;
 RA Chaing S., Clarke B., Sridhara S., Chu K., Friedman P., Vandusen W.,
 RA Roberts H.R., Blajchman M., Monroe D.M., High K.A.;
 RT "Severe factor VII deficiency caused by mutations abolishing the
 RT cleavage site for activation and altering binding to tissue factor.";
 RL Blood 83:3524-3535(1994).
 RN [16]
 RP VARIANT VAL-354.
 RX MEDLINE=95072589; PubMed=7981691;
 RA Bernardi F., Castaman G., Redaelli R., Pinotti M., Lunghi B.,
 RA Rodeghiero F., Marchetti G.;
 RT "Topologically equivalent mutations causing dysfunctional coagulation

RT factors VII (294Ala-->Val) and X (334Ser-->Pro).";
 RL Hum. Mol. Genet. 3:1175-1177(1994).
 RN [17]
 RP VARIANT MIE HIS-307.
 RX MEDLINE=95064662; PubMed=7974346;
 RA Ohiwa M., Hayashi T., Wada H., Minamikawa K., Shirakawa S.,
 RA Suzuki K.;
 RT "Factor VII M1e: homozygous asymptomatic type I deficiency caused by
 RT an amino acid substitution of His (CAC) for Arg(247) (CGC) in the
 RT catalytic domain.";
 RL Thromb. Haemost. 71:773-777(1994).
 RN [18]
 RP VARIANT MET-419.
 RX MEDLINE=96247510; PubMed=8652821;
 RA Arbini A.A., Mannucci P.M., Bauer K.A.;
 RT "A Thr359Met mutation in factor VII of a patient with a hereditary
 RT deficiency causes defective secretion of the molecule.";
 RL Blood 87:5085-5094(1996).
 RN [19]
 RP VARIANTS TRP-283; LYS-325; VAL-358; GLN-364; GLU-402 AND GLN-413.
 RX MEDLINE=97001216; PubMed=8844208;
 RA Bernardi F., Castaman G., Pinotti M., Ferraresi P., di Iasio M.G.,
 RA Lunghi B., Rodeghiero F., Marchetti G.;
 RT "Mutation pattern in clinically asymptomatic coagulation factor VII
 RT deficiency.";
 RL Hum. Mutat. 8:108-115(1996).
 RN [20]
 RP VARIANT VAL-304.
 RX MEDLINE=97037613; PubMed=8883260;
 RA Tamary H., Fromovich Y., Shalmon L., Reich Z., Dym O., Lanir N.,
 RA Brenner B., Paz M., Luder A.S., Blau O., Korostishevsky M.,
 RA Zaitov R., Seligsohn U.;
 RT "Ala244Val is a common, probably ancient mutation causing factor VII
 RT deficiency in Moroccan and Iranian Jews.";
 RL Thromb. Haemost. 76:283-291(1996).
 RN [21]
 RP VARIANT MORIOKA PRO-13.
 RX MEDLINE=9835713; PubMed=9576180;
 RA Ozawa T., Takikawa Y., Niiya K., Ejiri N., Suzuki K., Sato S.,
 RA Sakuragawa N.;
 RT "Factor VII Moriooka (FVII L-26P): a homozygous missense mutation in
 RT the signal sequence identified in a patient with factor VII
 RT deficiency.";
 RL Br. J. Haematol. 101:47-49(1998).
 RN [22]
 RP VARIANTS MALTA THR-194 AND VAL-304.
 RX MEDLINE=98112461; PubMed=9452082;
 RA Alshinawi C., Scerri C., Galdies R., Aquilina A., Felice A.E.;
 RT "Two new missense mutations (P134T and A244V) in the coagulation
 RT factor VII gene.";
 RL Hum. Mutat. Suppl. 1:S189-S191(1998).
 RN [23]
 RP VARIANTS ASP-295 AND GLN-413.
 RX MEDLINE=99318093; PubMed=10391209;
 RA Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
 RA Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,
 RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
 RA Lander E.S.;
 RT "Characterization of single-nucleotide polymorphisms in coding regions
 RT of human genes.";
 RL Nat. Genet. 22:231-238(1999).

Query Match 46.5%; Score 92; DB 1; Length 466;

Best Local Similarity 46.3%; Pred. No. 1.5e-07;

Matches 19; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

QY 1 ANSFLXVLRHSLSLFXKCYXTCDFXKXKXIFEDVDDTLAFW 41

|||||

Db 61 ANAFLELRPGSLERECKEQCSFEAREIFKDAERTKLFW 101

|||||

RESULT 13

TMGL_HUMAN

DR SMART; SMO0130; KR; 2.
DR PROSITE; PS00020; TRYP_SPC; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
DR PROSITE; PS00021; KRINGLE_1; 2.
DR PROSITE; PS00070; KRINGLE_2; 2.
DR PROSITE; PS00240; TRYP_SIN_DOM; 1.
DR PROSITE; PS00134; TRYP_SIN_DOM; 1.
DR PROSITE; PS00135; TRYP_SIN_SER; 1.
KW Blood coagulation: Plasma Calcium-binding; Glycoprotein; Repeat;
KW Vitamin K; Zymogen; Gamma-carboxyglutamic acid; Acute phase; Liver;
KW Hydrolase; Serine protease; Kringle; Signal.
FT SIGNAL 1 24
FT PROPEP 25 43
FT CHAIN 44 617
FT PEPTIDE 44 200
FT PEPTIDE 201 323
FT PEPTIDE 324 359
FT CHAIN 360 617
FT CHAIN 109 187
FT DOMAIN 215 292
FT DOMAIN 360 617
FT SITE 200 201
FT SITE 323 324
FT SITE 359 360
FT SITE 402 402
FT ACT_SITE 458 458
FT ACT_SITE 564 564
FT MOD_RES 50 50
FT MOD_RES 51 51
FT MOD_RES 58 58
FT MOD_RES 60 60
FT MOD_RES 63 63
FT MOD_RES 64 64
FT MOD_RES 69 69
FT MOD_RES 70 70
FT MOD_RES 73 73
FT MOD_RES 76 76
FT CARBOHYD 120 120
FT CARBOHYD 144 144
FT CARBOHYD 412 412
FT CARBOHYD 552 552
FT DISULFID 61 66
FT DISULFID 91 104
FT DISULFID 109 187
FT DISULFID 130 170
FT DISULFID 158 182
FT DISULFID 215 292
FT DISULFID 236 276
FT DISULFID 264 287
FT DISULFID 332 478
FT DISULFID 387 403
FT DISULFID 532 546
FT DISULFID 560 590
SQ SEQUENCE 617 AA; AD27DIB71445DBID CRC64;
Query Match 39.6%; Score 78.5; DB 1; Length 617;
Best local similarity 40.0%; Pred. No. 3.7e-05;
Matches 18; Conservative 5; Mismatches 21; Indels 1; Gaps 1;
QY 1 ANS-FLXLRHSSLRXCIXICDPFXAXXIFEDVDITAFWSKH 44
Db 44 ANSGFLELRGNLERECVCEQSYEAFEALESPOQTDVFWAKY 88
RESULT 15
ID_THRB_MOUSE STANDARD; PRT; 618 AA.
AC P19221;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Prothrombin precursor (EC 3.4.21.5).
GN F2 OR CF2.

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Liver;
RX MEDLINE=91025551; PubMed=2222810;
RA Fritzenberg Degen S.J., Schaffer L.A., Jamison C.S., Grant S.G.,
RA Fitzgibbon J.J., Pai J.-A., Chapman V.M., Elliott R.W.;
RT "Characterization of the cDNA coding for mouse prothrombin and
RT localization of the gene on mouse chromosome 2.";
RL DNA Cell Biol. 9:487-498(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Locuallano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McQuellano P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.B.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE OF 394-618 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=92212913; PubMed=1557383;
RA Banfield D.K., Macgillivray R.T.;
RT "Partial characterization of vertebrate prothrombin cDNAs:
RT amplification and sequence analysis of the B chain of thrombin from
RT nine different species";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
CC -!- FUNCTION: Thrombin, which cleaves bonds after Arg and Lys,
CC converts fibrinogen to fibrin and activates factors V, VII, VIII,
CC XIII, and, in complex with thrombomodulin, protein C.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-Gly; activates
CC fibrinogen to fibrin and releases fibrinopeptide A and B.
CC -!- PTM: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,
CC RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL
CC ENZYME, THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES
CC ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY
CC CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION
CC OF PROTHROMBIN TO THROMBIN.
CC -!- MISCELLANEOUS: Prothrombin is activated on the surface of a
CC phospholipid membrane that binds the amino end of prothrombin and
CC factors Va and Xa in Ca-dependent interactions; factor Xa removes
CC the activation peptide and cleaves the remaining part into light
CC and heavy chains. The activation process starts slowly because
CC factor V itself has to be activated by the initial, small amounts
CC of thrombin.
CC -!- MISCELLANEOUS: Thrombin can itself cleave the amino terminal
CC fragment (fragment 1) of the prothrombin, prior to its activation
CC by factor Xa.
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- SIMILARITY: Contains 2 kringle domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its

use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announcement/> or send an email to license@isb-sib.ch).

ENBL; X52308; CAA36548.1; -;
DR EMBL; BC013662; AAH13662.1; -;
DR EMBL; MG1394; AAA40435.1; -;
DR FIR; A35827; A35827.
DR HSSP; P00734; 1B7X.
DR MEROPS; S01.217; -.
DR MGD; MG1:88380; F2.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR003966; Peptidase_S1A_pr.
DR InterPro; IPR000234; Vita_dep_GLA.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00051; Kringle; 2.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PRO0722; CHYMOTRYPSIN.
DR PRINTS; PRO0001; GLABLOOD.
DR PRINTS; PRO0018; KRINGLE.
DR PRINTS; PRO1505; PROTHROMBIN.
DR ProDom; PD000395; Kringle; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00130; KR; 2.
DR SMART; SM00020; TRYPSIN; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
DR PROSITE; PS00021; KRINGLE_1; 2.
DR PROSITE; PS00070; KRINGLE_2; 2.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Blood coagulation; Plasma; Calcium-binding; Glycoprotein; Repeat;
KW Vitamin K; Zymogen; Gamma-carboxyglutamic acid; Acute phase; Liver;
KW Hydrolase; Serine protease; Kringle; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT PROPEP 25 43
FT CHAIN 44 618 PROTHROMBIN.
FT PEPTIDE 44 200 ACTIVATION PEPTIDE (FRAGMENT 1).
FT PEPTIDE 201 324 ACTIVATION PEPTIDE (FRAGMENT 2).
FT CHAIN 325 360 THROMBIN LIGHT CHAIN (A).
FT CHAIN 361 618 THROMBIN HEAVY CHAIN (B).
FT DOMAIN 109 187 KRINGLE 1.
FT DOMAIN 215 292 KRINGLE 2.
FT DOMAIN 361 618 SERINE PROTEASE.
FT SITE 200 201 CLEAVAGE (BY THROMBIN).
FT SITE 324 325 CLEAVAGE (BY FACTOR XA).
FT SITE 360 361 CLEAVAGE (BY FACTOR XA).
FT ACT_SITE 403 403 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 459 459 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 565 565 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT MOD_RES 50 50 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 51 51 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 58 58 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 63 63 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 64 64 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 69 69 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 73 73 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 76 76 GAMMA-CARBOXYGLUTAMIC ACID.
FT DISULFID 61 66 BY SIMILARITY.
FT DISULFID 91 104 BY SIMILARITY.
FT DISULFID 109 187 BY SIMILARITY.
FT DISULFID 130 170 BY SIMILARITY.
FT DISULFID 158 182 BY SIMILARITY.
FT DISULFID 215 293 BY SIMILARITY.
FT DISULFID 236 276 BY SIMILARITY.
FT DISULFID 264 288 BY SIMILARITY.

FT DISULFID 333 479
FT DISULFID 388 404
FT DISULFID 533 547
FT DISULFID 561 591
FT CARBOHYD 122 122
FT CARBOHYD 144 144
FT CARBOHYD 413 413
FT CARBOHYD 553 553
SQ SEQUENCE 618 AA; 70268 MW; 10:03:23

Query Match 39.6%; Score
Best Local Similarity 40.0%; Pred.
Matches 18; Conservative 5; Mis

Qy 1 ANS-FLXXLRHSSILXRCIXXICDPXX
Db 44 ANSGFLELRKGNLRECVBEQCSYEAFAL

Search completed: March 1, 2004, 10:03:23
Job time : 11.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2004, 09:55:12 ; Search time 37.5 Seconds
(without alignments)
370.208 Million cell updates/sec

Title: SEQ1-32GLU-33ASP

Perfect score: 198

Sequence: 1 ANSFLXLRHSLRXRCIXX.....XXAKXIFVDVDTLAFWSKH 44

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL.25.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phage.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	144	72.7	456	Q9TTR0	Q9TTR0 canis famil
2	133	67.2	460	Q31WN8	Q31WN8 mus musculus
3	130	65.7	55	Q8J002	Q8J002 homo sapien
4	130	65.7	55	Q8IXB5	Q8IXB5 homo sapien
5	127	64.1	460	Q99PC6	Q99PC6 mus musculus
6	107	54.0	482	Q63207	Q63207 rattus norv
7	102	51.5	455	Q7SY86	Q7SY86 xenopus lae
8	100	50.5	433	Q804X6	Q804X6 gallus gall
9	98	48.7	524	Q7SXH8	Q7SXH8 brachydanio
10	96.5	48.7	443	Q8JHC9	Q8JHC9 brachydanio
11	96	48.5	231	Q8NZN6	Q8NZN6 homo sapien
12	93	47.0	340	Q80Y26	Q80Y26 mus musculus
13	93	47.0	434	Q7T3B6	Q7T3B6 brachydanio
14	93	47.0	481	O54740	O54740 mus musculus
15	93	47.0	481	Q9L132	Q9L132 mus musculus
16	93	47.0	481	O88947	O88947 mus musculus

17	92	46.5	679	4	Q86PQ8	Q86PQ8 homo sapien
18	89	44.9	474	13	Q8JHC8	Q8JHC8 brachydanio
19	88.5	44.7	442	13	Q804X1	Q804X1 fugu rubrip
20	87	43.9	469	6	Q9GMD9	Q9GMD9 ornithorhyn
21	82	41.4	229	13	Q8JU40	Q8JU40 xenopus lae
22	81	40.9	268	4	Q8NEK6	Q8NEK6 homo sapien
23	80	40.4	425	13	Q804X7	Q804X7 gallus gall
24	80	40.4	612	13	Q804W7	Q804W7 fugu rubrip
25	79	39.9	446	11	Q8K3U6	Q8K3U6 rattus norv
26	76	38.4	100	4	Q152S3	Q152S3 homo sapien
27	76	38.4	622	4	Q7Z7P3	Q7Z7P3 homo sapien
28	74	37.4	471	13	Q804X6	Q804X6 gallus gall
29	74	37.4	475	13	Q804W9	Q804W9 fugu rubrip
30	74	37.4	497	4	Q7Z7I5	Q7Z7I5 homo sapien
31	74	37.4	650	4	Q165I9	Q165I9 homo sapien
32	74	37.4	650	4	Q9NSD0	Q9NSD0 homo sapien
33	73	36.9	446	11	Q61109	Q61109 mus musculu
34	71.5	36.1	542	5	Q8T6I3	Q8T6I3 halocynthia
35	71	35.9	138	6	Q28994	Q28994 sus scrofa
36	71	35.9	441	13	Q804X2	Q804X2 fugu rubrip
37	70	35.4	607	13	Q91001	Q91001 gallus gall
38	69	34.8	461	6	Q95ND7	Q95ND7 pan troglod
39	69	34.8	461	6	Q95ND6	Q95ND6 pan troglod
40	67	33.8	648	6	Q29094	Q29094 sus scrofa
41	66.5	33.6	433	13	Q8JHD0	Q8JHD0 brachydanio
42	66.5	33.6	433	13	Q90YK1	Q90YK1 brachydanio
43	66	33.3	49	6	Q95ME8	Q95ME8 bos taurus
44	66	33.3	52	4	Q8IXD5	Q8IXD5 homo sapien
45	64	32.3	430	13	Q804X0	Q804X0 fugu rubrip

ALIGNMENTS

RESULT 1

Q9TTR0	AC	Q9TTR0	PRELIMINARY;	PRT;	456 AA.
ID	Q9TTR0;				
DT	01-MAY-2000 (TRENBLrel. 13, Created)				
DT	01-MAY-2000 (TRENBLrel. 13, Last sequence update)				
DT	01-OCT-2003 (TRENBLrel. 25, Last annotation update)				
DB	Protein C precursor.				
GN	PROC.				
OS	Canis familiaris (Dog).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OX	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.				
NCBI_TaxID=9615;					
[1]	SEQUENCE FROM N.A.				
Leeb T., Kopp T., Deppe A., Breen M., Matis U., Brunnberg L.,					
Brenig B.;					
"Molecular characterization and chromosomal assignment of the canine					
protein C gene."					
Mamm. Genome 10:135-139(1999).					
[2]	SEQUENCE FROM N.A.				
MEDLINE=9371952; Pubmed=10443005;					
Leeb T., Pfeiffer I., Kopp T., Deppe A., Brenig B.;					
"Analysis of canine protein C gene polymorphisms."					
Anim. Genet. 30:237-238(1999).					
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.					
EMBL; AJ001979; CAA05126.1; -					
HSP; P04070; IAUU					
GO; GO:0005576; C:extracellular; IEA.					
GO; GO:0005509; F:calcium ion binding; IEA.					
GO; GO:0004263; F:chymotrypsin activity; IEA.					
GO; GO:0008233; F:peptidase activity; IEA.					
GO; GO:0004295; F:trypsin activity; IEA.					
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.					
InterPro; IPR000152; Asx_hydroxyl_s.					
InterPro; IPR009003; Cys_Ser_trypsin.					
InterPro; IPR001881; EGF_Ca.					
InterPro; IPR006209; EGF_like.					

DR InterPro; IPR002383; GLA blood.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; Gla; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SMC0179; EGF_CA; 1.
DR SMART; SMC0069; GLA; 1.
DR SMART; SMC0020; TRYPSIN_SPC; 1.
DR PROSITE; PS00010; ASX HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS01134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR EGF-like domain; Hydrolase; Protease; Serine protease; Signal.
FT SIGNAL 1 42 POTENTIAL.
FT CHAIN 43 192 PROTEIN C LIGHT CHAIN.
FT CHAIN 193 194 PROTEIN C CONNECTING DIPEPTIDE.
FT CHAIN 195 456 PROTEIN C HEAVY CHAIN.
SQ SEQUENCE 456 AA; 50813 MW; 7AD3A8C1C34E59FF CRC64;

Query Match 72.7%; Score 144; DB 6; Length 456;
Best Local Similarity 61.4%; Pred. No. 9.3e-16;
Matches 27; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 1 ANSFLXLRHSLRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
DB 43 ANSFLFIRAGSLRECEMEEICDFEAKEIFQNVDDTLAYWSKY 86

RESULT 2

ID Q91WN8 PRELIMINARY; PRT; 460 AA.
AC Q91WN8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to protein C.
GN PROC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10990;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; BC013896; AAH13896.1; -.
DR HSSP; P00761; 1ANI.
DR MGD; MGI:97771; Proc.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0006233; F:peptidase activity; IEA.
DR GO; GO:0004292; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR00152; ASX hydroxyl S.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR01881; EGF_Ca.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR002383; GLA blood.
DR InterPro; IPR01254; Peptidase S1.
DR InterPro; IPR001314; Peptidase S1A.
DR InterPro; IPR000294; VitK_dep_GLA.

DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; Gla; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SMC0179; EGF_CA; 1.
DR SMART; SMC0069; GLA; 1.
DR SMART; SMC0020; TRYPSIN_SPC; 1.
DR PROSITE; PS00010; ASX HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS01134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR EGF-like domain; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 460 AA; 51818 MW; 0117F2E5E68FCC274 CRC64;

Query Match 67.2%; Score 133; DB 11; Length 460;
Best Local Similarity 56.8%; Pred. No. 6.9e-14;
Matches 25; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANSFLXLRHSLRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
DB 42 ANSFLFIRAGSLRECEMEEICDFEAKEIFQNVDDTLAFWIKY 85

RESULT 3

Q8J002 PRELIMINARY; PRT; 55 AA.
AC Q8J002;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Protein C (Fragment).
GN PROC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kinoshita S., Iida H., Inoue S., Watanabe K., Kurihara M., Wada Y.,
RA Ono M., Dongchon K., Hamasaki N.;
RT "Gene Analysis of Anticoagulation Factors in Japanese Thrombotic
RT Patients. Genetic Background of Thrombophilia in Japan."
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB083700; BAC21172.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR002383; GLA blood.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00594; Gla; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SMC0069; GLA; 1.
FT NON TER 1
FT NON TER 55
SQ SEQUENCE 55 AA; 6527 MW; 4F89496534A78836 CRC64;

Query Match 65.7%; Score 130; DB 4; Length 55;
Best Local Similarity 70.3%; Pred. No. 2.2e-14;
Matches 26; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 ANSFLXLRHSLRXCIXXICDFXXAKXIFEDVDDT 37
DB 19 ANSFLKELRHSLECEIEICDFEAKEIFQNVDDT 55

RESULT 4

Q8IXB5 PRELIMINARY; PRT; 55 AA.
ID Q8IXB5
AC Q8IXB5;

```
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Protein C (Fragment).
GN PROCI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RA Hamaaki S., Kang D., Kinoshita S., Iida K., Inoue S., Watanabe K.,
RA Kurihara M., Wada Y., Ono M.;
RT "Gene analysis of anticoagulation factors in Japanese thrombotic
RT patients.Genetic background of thrombophilia in Japan.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL, AB086851; BAC53631.1;
DR GO, GO:0005576; C:extracellular; IEA.
DR GO, GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR002393; GLA blood.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00069; GLA; 1.
FT NON_TER 1 55.
FT NON_TER 55.
SQ SEQUENCE 55 AA; 6475 MW; 3803696534BC9289 CRC64;

Query Match 65.7%; Score 130; DB 4; Length 55;
Best Local Similarity 70.3%; Pred. No. 2,2e-14;
Matches 26; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 ANSFLXLRHSLRXCIXICDPXXAKXIFEDVDDT 37
DB 19 ANSFLFELRHSLRECEIEICDPFEAKEIFQNVDDT 55

RESULT 5
Q99PC6 PRELIMINARY; PRT; 460 AA.
ID Q99PC6;
AC Q99PC6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anticoagulant protein C.
GN PROC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL;
RA Korf I.;
RT "Complete sequence of UC72A01.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AF318182; AAK07918.1; -.
DR HSSP; P04070; 1AUT.
DR MGP; MGI:87771; Proc.
DR GO, GO:0005576; C:extracellular; IEA.
DR GO, GO:0005509; F:calcium ion binding; IEA.
DR GO, GO:0004263; F:chymotrypsin activity; IEA.
DR GO, GO:0008233; F:peptidase activity; IEA.
DR GO, GO:0004295; F:trypsin activity; IEA.
DR GO, GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR00152; Asx_hydroxyl_S.
DR InterPro; IPR009003; Cys_ser_trypsin.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002383; GLA blood.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase_S1a.
DR InterPro; IPR001314; Peptidase_S1a.
```

```
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00089; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR EGF-like domain; Hydrolase; Protease; Serine protease.
KW EGF-like domain; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 460 AA; 51784 MW; 0293BC25E9D3ED16 CRC64;

Query Match 64.1%; Score 127; DB 11; Length 460;
Best Local Similarity 54.5%; Pred. No. 7,2e-13;
Matches 24; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

QY 1 ANSFLXLRHSLRXCIXICDPXXAKXIFEDVDDT 44
DB 42 ANSFLFELRHSLRECEIEICDPFEAKEIFQNVDDT 85

RESULT 6
Q63207 PRELIMINARY; PRT; 482 AA.
ID Q63207;
AC Q63207;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Factor X.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_TaxID=10116;
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=96093366; PubMed=8578539;
RA Stanton C., Ross R.P., Hutson S., Wallin R.;
RT "Evidence for competition between vitamin K-dependent clotting factors
RT for intracellular processing by the vitamin K-dependent gamma-
RT carboxylase.";
RL Thromb. Res. 80:63-73(1995).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; X79807; CAA56202.1; -.
DR PIR; S49075; EXRT.
DR HSSP; P00742; 1XKA.
DR MEROPS; S01.216; -.
DR GO, GO:0005576; C:extracellular; IEA.
DR GO, GO:0005509; F:calcium ion binding; IEA.
DR GO, GO:0004263; F:chymotrypsin activity; IEA.
DR GO, GO:0008233; F:peptidase activity; IEA.
DR GO, GO:0004295; F:trypsin activity; IEA.
DR GO, GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR00152; Asx_hydroxyl_S.
DR InterPro; IPR009003; Cys_ser_trypsin.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002383; GLA blood.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase_S1a.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
```

```
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGFBL00D.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA_1.
DR SMART; SM00020; TRY2_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW EGF-like domain; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 482 AA; 54265 MW; 0284678E3954A698 CRC64;

Query Match 54.0%; Score 107; DB 11; Length 482;
Best Local Similarity 40.9%; Pred. No. 1.9e-09;
Matches 18; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 1 ANSFLXLRHSSLRKXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
   ||||| : : : : : ||||| : : : : : ||||| : : : : :
Db 41 ANSFFFEIKGNLERECVCEICSFEEAREVFEDNKTETFWNKY 84

RESULT 7
Q7SY86
ID Q7SY86 PRELIMINARY; PRT; 455 AA.
AC Q7SY86;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RX MEDLINE=2231132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Schmutz E.D., Dickson M.C.,
RA Rodriguez A.C., Guichwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
```

```
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RA Klein S., Strausberg R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
KW Hypothetical protein.
SQ SEQUENCE 455 AA; 51811 MW; 07C027ED2B495330 CRC64;

Query Match 51.5%; Score 102; DB 13; Length 455;
Best Local Similarity 47.7%; Pred. No. 1.3e-08;
Matches 21; Conservative 6; Mismatches 17; Indels 0; Gaps 0;

QY 1 ANSFLXLRHSSLRKXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
   ||||| : : : : : ||||| : : : : : ||||| : : : : :
Db 49 AFNFMWELKPGSLERECIEKCDFEAEFIEFTKEDTLNFWAKY 92

RESULT 8
Q804X5
ID Q804X5 PRELIMINARY; PRT; 433 AA.
AC Q804X5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anticoagulant protein C precursor (EC 3.4.21.69).
GN PROC.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Davidson C.J., Hirt R.P., Lal K., Snell P., Elgar G.,
RA Tuddenham E.G.D., McVey J.H.;
RT "Comparative sequence analysis and molecular evolution of blood
RT coagulation genes from Gallus gallus and Eugu rubripes.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF465270; AAC33365.1; -.
DR GO; GO:0005576; A:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0003808; F:protein C (activated) activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR00742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRY2_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
```

```
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase.
SQ SEQUENCE 433 AA; 48689 MW; E09DDE56D7DA2A3 CRC64;

Query Match
Best Local Similarity 50.5%; Score 100; DB 13; Length 433;
Matches 21; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

QY 1 ANSFLXLRHSSLRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 40 ANSFLXLRHSSLRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 83
||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 9
ID Q7SXH8 PRELIMINARY; PRT; 524 AA.
AC Q7SXH8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Body;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Lequellano N.A., Peters G.J., Carninci P., Prange C.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullany S.J.,
RA Villalón D.K., Muzny K.C., Hale S.D., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Body;
RA Strausberg R.;
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC055596; AAH55596.1; -.
KW Hypothetical protein.
SQ SEQUENCE 524 AA; 59560 MW; 1BAAE08119080325 CRC64;

Query Match
Best Local Similarity 49.5%; Score 98; DB 13; Length 524;
Matches 18; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

QY 1 ANSFLXLRHSSLRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 42 ANTVEELKPGNLERECVEECIDHEAREVERVDKTEIFWKY 85
||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
Q8JHC9
ID Q8JHC9 PRELIMINARY; PRT; 443 AA.
AC Q8JHC9;
DT 01-OCT-2003 (TrEMBLrel. 22, Created)
```

```
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Coagulation factor VIII.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RT "Comprehensive analysis of blood coagulation pathways in Teleostei:
RT Evolution of coagulation factor genes and identification of zebrafish
RT factor VIII."
EL Blood Cells Mol. Dis. 0:0-0(2002).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AF519546; AAM88342.1; -.
DR EMBL; AF515269; AAN71000.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004363; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR00742; EGF-2.
DR InterPro; IPR01881; EGF_Ca.
DR InterPro; IPR06209; EGF_like.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR01254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00594; GLA; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYD_SPC; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
KW EGF-like domain; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 443 AA; 48823 MW; 2D2504718AE94FF4 CRC64;

Query Match
Best Local Similarity 48.7%; Score 96.5; DB 13; Length 443;
Matches 19; Conservative 7; Mismatches 15; Indels 1; Gaps 1;

QY 1 ANSFLXLRHSSLRXCIXXICDFXXAKXIFEDVDDTLAFW 41
||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 38 ANSGLFLEMKAGNLERECVEECIDYEAREVEFDDRTKQFW 79
||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 11
Q8NZNG
ID Q8NZNG PRELIMINARY; PRT; 231 AA.
AC Q8NZNG;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ90093.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
```

```

RC TISSUE=Embryo;
RA Isoqai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,
RA Masuho Y., Ono S., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK074574; BAC11069.1; -
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00594; Gla; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
KW Hypothetical protein.
SQ SEQUENCE 231 AA; 28844 MW; 8A373B0D5C1D0D81 CRC64;

Query Match 48.5%; Score 96; DB 4; Length 231;
Best Local Similarity 39.0%; Pred. No. 6.3e-08;
Matches 16; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 1 ANSFLXLRHSSLRXCIXXICDFXKXKXIFEDVDDTLAFW 41
DB 20 ANSFLEELRGTTIERECWEEICSYEEVKEVFENKXETMEFW 60

RESULT 12
Q80Y26 PRELIMINARY; PRT; 340 AA.
AC Q80Y26;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE F10 protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., McKernan K.J., Abramson R.D., Mullaly S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX Strausberg R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC050219; AAH50219.1; -
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.

```

```

DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.
DR InterPro; IPR00152; Asx_hydroxyl_S.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; Gla; 1.
DR PRINTS; PR00010; EGFBLOOD.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
SQ SEQUENCE 340 AA; 38359 MW; EE252D6157720811 CRC64;

Query Match 47.0%; Score 93; DB 11; Length 340;
Best Local Similarity 36.4%; Pred. No. 3.1e-07;
Matches 16; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANSFLXLRHSSLRXCIXXICDFXKXKXIFEDVDDTLAFWSKH 44
DB 53 ANSPFEEFKGNLERECWEEICSYEEVKEVFEDDEKTKYWTKY 96

RESULT 13
Q7T3B6 PRELIMINARY; PRT; 434 AA.
AC Q7T3B6;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";

```

```

DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPsin DOM; 1.
DR PROSITE; PS00134; TRYPsin_HIS; 1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
KW EGF-like domain; Hydrolase; Protease; Serine protease; Signal;
KW Plasminid.
FT SIGNAL
FT CHAIN
SQ SEQUENCE 481 AA; 53986 MW; CF702DESEFD97AE CRC64;

Query/Match
Best Local Similarity 47.0%; Score 93; DB 11; Length 481;
Matches 16; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANSFLLXLRHSLRXCTIXICDFXXAKXIFEDVDDTLAFWSKH 44
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 41 ANSFEEFKGNLRCEWESICSYEEVRIFEDDEKTYWTKY 84

RESULT 15
Q99L32
ID Q99L32 PRELIMINARY; PRT; 481 AA.
AC Q99L32;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Coagulation factor X.
GN FN10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
OC NCBI_TaxID=10090;
RN [1]
RP STRAUSBERG R.;
RA Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; BC003877; AA03877.1; -.
DR HSSP; P00742; 1XKA.
DR MEROPS; S01.216; -.
DR MGD; MGI:103107; F10.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0006233; F:peptidase activity; IEA.
DR GO; GO:0004235; F:trypsin activity; IEA.
DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000152; Asx hydroxyl S.
DR InterPro; IPR009003; Cys Ser _trypsin.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001436; EGF_I1.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGF_blood.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.

```


GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2004, 10:03:28 ; Search time 16.5 Seconds
(without alignments)
137.669 Million cell updates/sec

Title: SEQ1-32GLU-33ASP

Perfect score: 198

Sequence: 1 ANSFLXLRHSLRXCIIX.....XXAKXIFEDVDTLAFWSKH 44

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PTCUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	180	90.9	44	3	US-08-955-636-19
2	176	88.9	419	4	US-10-182-263-3
3	176	88.9	419	4	US-10-182-263-4
4	176	88.9	419	4	US-10-182-263-5
5	172	86.9	44	3	US-08-955-636-1
6	172	86.9	44	3	US-08-955-636-20
7	172	86.9	44	3	US-08-955-636-21
8	172	86.9	44	3	US-08-955-636-25
9	172	86.9	45	2	US-08-965-832-2
10	172	86.9	419	1	US-08-295-411-1
11	172	86.9	419	2	US-08-955-471-1
12	172	86.9	419	4	US-08-667-570A-3
13	172	86.9	419	4	US-10-182-263-1
14	172	86.9	419	5	PCT-US92-10242-1
15	172	86.9	460	2	US-08-756-506-2
16	172	86.9	460	2	US-08-756-506-4
17	172	86.9	460	6	5270178-13
18	172	86.9	460	6	5270178-14
19	172	86.9	460	6	5270178-15
20	172	86.9	460	6	5270178-16
21	172	86.9	461	4	US-10-182-263-2
22	172	86.9	461	6	5225537-2
23	172	86.9	461	6	5270178-17
24	172	86.9	461	6	5270178-18
25	172	86.9	461	6	5460953-3
26	171	86.4	44	3	US-08-955-636-22
27	168	84.8	44	3	US-08-955-636-24

28 1 168 84.8 44 3 US-08-955-636-35 Sequence 35, Appl
29 168 84.8 419 4 US-10-182-263-6 Sequence 6, Appl
30 159 80.3 42 2 US-08-745-254A-2 Sequence 2, Appl
31 159 80.3 461 6 5270178-2 Patent No. 5270178
32 155 78.3 41 1 US-08-229-280-5 Sequence 5, Appl
33 150 75.8 42 4 US-09-383-667-8 Sequence 8, Appl
34 141 71.2 410 3 US-09-065-872-1 Sequence 1, Appl
35 141 71.2 410 4 US-09-667-570A-1 Sequence 1, Appl
36 133 67.2 409 3 US-09-065-872-2 Sequence 2, Appl
37 133 67.2 409 4 US-09-667-570A-2 Sequence 2, Appl
38 119 60.1 44 3 US-08-955-636-23 Sequence 23, Appl
39 109 55.1 44 3 US-08-955-636-2 Sequence 2, Appl
40 106 53.5 139 1 US-08-330-978-2 Sequence 2, Appl
41 106 53.5 139 1 US-08-474-042-2 Sequence 2, Appl
42 106 53.5 139 1 US-08-484-558-2 Sequence 2, Appl
43 106 53.5 139 1 US-08-774-592-2 Sequence 2, Appl
44 106 53.5 437 1 US-08-487-037-2 Sequence 2, Appl
45 106 53.5 437 1 US-08-487-037-3 Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-955-636-19
; Sequence 19, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelsaestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic acid
US-08-955-636-19

Query Match 90.9%; Score 180; DB 3; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.4e-23;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANSFLXLRHSLRXCIIXICDFXXAKXIFEDVDTLAFWSKH 44
Db 1 ANSFLXLRHSLRXCIIXICDFXXAKXIFEDVDTLAFWSKH 44

RESULT 2
US-10-182-263-3
; Sequence 3, Application US/10182263
; Patent No. 6630138
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; PRIOR FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1


```
; SEQ ID NO 3
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-3

Query Match      88.9%; Score 176; DB 4; Length 419;
Best Local Similarity 77.3%; Pred. No. 9.3e-22;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANSFLXLRHSSLRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 ANSFLELRHSGSLRECEICDFEAKEIFEDVDDTLAFWSKH 44

RESULT 3
US-10-182-263-4
; Sequence 4, Application US/10182263
; Patent No. 6630138
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-4

Query Match      88.9%; Score 176; DB 4; Length 419;
Best Local Similarity 77.3%; Pred. No. 9.3e-22;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANSFLXLRHSSLRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 ANSFLELRHSGSLRECEICDFEAKEIFEDVDDTLAFWSKH 44

RESULT 4
US-10-182-263-5
; Sequence 5, Application US/10182263
; Patent No. 6630138
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-5

Query Match      88.9%; Score 176; DB 4; Length 419;
```

```
Best Local Similarity 77.3%; Pred. No. 9.3e-22;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANSFLXLRHSSLRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 ANSFLELRHSGSLRECEICDFEAKEIFEDVDDTLAFWSKH 44

RESULT 5
US-08-955-636-1
; Sequence 1, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: POLYPEPTIDES
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic acid
US-08-955-636-1

Query Match      86.9%; Score 172; DB 3; Length 44;
Best Local Similarity 95.5%; Pred. No. 3.3e-22;
Matches 42; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANSFLXLRHSSLRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 ANSFLLXLRHSSLRXCIXXICDFXXAKXIFQNVDDTLAFWSKH 44

RESULT 6
US-08-955-636-20
; Sequence 20, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: POLYPEPTIDES
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic acid
US-08-955-636-20

Query Match      86.9%; Score 172; DB 3; Length 44;
Best Local Similarity 97.7%; Pred. No. 3.3e-22;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANSFLXLRHSSLRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 ANSFLLXLRHSSLRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44

RESULT 7
```

08-955-636-21
Sequence 21, Application US/08955636A
Patent No. 6017882

GENERAL INFORMATION:
APPLICANT: Nelsetuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
POLYPEPTIDES
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 21
LENGTH: 44
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic acid
-08-955-636-21

Query Match 86.9%; Score 172; DB 3; Length 44;
Best Local Similarity 97.7%; Pred. No. 3.3e-22;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 ANSFLXLRHSSLRXCIXXICDPXXAKXIFEDVDOTLAFWSKH 44
1 ANSFLXLRHSSLRXCIXXICDPXXAKXIFEDVDOTLAFWSKH 44

RESULT 8

US-08-955-636-25
Sequence 25, Application US/08955636A
Patent No. 6017882
GENERAL INFORMATION:

APPLICANT: Nelsetuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
POLYPEPTIDES
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 25
LENGTH: 44
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic acid
US-08-955-636-25

Query Match 86.9%; Score 172; DB 3; Length 44;
Best Local Similarity 97.7%; Pred. No. 3.3e-22;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ANSFLXLRHSSLRXCIXXICDPXXAKXIFEDVDOTLAFWSKH 44
Db 1 ANSFLXLRHSSLRXCIXXICDPXXAKXIFEDVDOTLAFWSKH 44

RESULT 9

US-08-965-832-2
Sequence 2, Application US/08965832
Patent No. 5847085
GENERAL INFORMATION:
APPLICANT: CHARLES T. ESMON AND MIKHAIL D. SMIRNOV
TITLE OF INVENTION: Modified Protein C
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst

STREET: 2800 One Atlantic Center, 1201 West
STREET: Peachtree Street
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/965,832
FILING DATE: 7-NOV-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/745,254
FILING DATE: 8-NOV-1996
APPLICATION NUMBER: 60/053,768
FILING DATE: 25-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION/DOCKET NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF 165/167
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-873-8795
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29
OTHER INFORMATION: /note= "where Xaa means gamma
OTHER INFORMATION: carboxyglutamic acid"
FEATURE:
NAME/KEY:
LOCATION:
OTHER INFORMATION: /note= "partial sequence of human protein C"
US-08-965-832-2

Query Match 86.9%; Score 172; DB 2; Length 45;
Best Local Similarity 95.5%; Pred. No. 3.3e-22;
Matches 42; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANSFLXLRHSSLRXCIXXICDPXXAKXIFEDVDOTLAFWSKH 44
Db 1 ANSFLXLRHSSLRXCIXXICDPXXAKXIFEDVDOTLAFWSKH 44

RESULT 10

US-08-295-411-1
Sequence 1, Application US/08295411
Patent No. 5679639
GENERAL INFORMATION:

APPLICANT: Griffin, John H.
APPLICANT: Masters, Rolf M.
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
Anti-Peptide Antibodies, Systems and Therapeutic Methods
for Inhibiting Coagulation
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Office of Patent Counsel, The Scripps
ADDRESSEE: Research Institute
STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA

ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/295,411
FILING DATE: 22-AUG-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,989
FILING DATE: 18-NOV-1991
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI263.0C1
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Region
LOCATION: 1..157
OTHER INFORMATION: /note= "Protein C Light Chain"
FEATURE:
NAME/KEY: Region
LOCATION: 158..169
OTHER INFORMATION: /note= "Protein C Activation"
OTHER INFORMATION: Peptide"
FEATURE:
NAME/KEY: Region
LOCATION: 170..419
OTHER INFORMATION: /note= "Protein C Heavy Chain"
US-08-295-411-1
Query Match 86.9%; Score 172; DB 1; Length 419;
Best Local Similarity 75.0%; Pred. No. 4.5e-21;
Matches 33; Conservative 2; Mismatches 9; Indels 0; Gaps 0;
QY 1 ANSFLLXLRHSSLRXCIXXICDFXAKXIFEDVDDTLAFWSKH 44
Db 1 ANSFLELRHSSLRXCIEICDFEAKEIFQNVDDTLAFWSKH 44
RESULT 11
US-08-955-471-1
Sequence 1, Application US/08955471
Patent No. 5968751
GENERAL INFORMATION:
APPLICANT: Griffin, John K.
APPLICANT: Westers, Rolf M.
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: for Inhibiting Coagulation
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: Office of Patent Counsel, The Scripps
ADDRESSER: Research Institute
STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/955,471
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/295,411
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI263.0C1
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Region
LOCATION: 1..157
OTHER INFORMATION: /note= "Protein C Light Chain"
FEATURE:
NAME/KEY: Region
LOCATION: 158..169
OTHER INFORMATION: /note= "Protein C Activation"
OTHER INFORMATION: Peptide"
FEATURE:
NAME/KEY: Region
LOCATION: 170..419
OTHER INFORMATION: /note= "Protein C Heavy Chain"
US-08-955-471-1
Query Match 86.9%; Score 172; DB 2; Length 419;
Best Local Similarity 75.0%; Pred. No. 4.5e-21;
Matches 33; Conservative 2; Mismatches 9; Indels 0; Gaps 0;
QY 1 ANSFLLXLRHSSLRXCIXXICDFXAKXIFEDVDDTLAFWSKH 44
Db 1 ANSFLELRHSSLRXCIEICDFEAKEIFQNVDDTLAFWSKH 44
RESULT 12
US-08-667-570A-3
Sequence 3, Application US/09667570A
Patent No. 6436397
GENERAL INFORMATION:
APPLICANT: Baker, Jeffrey C
APPLICANT: Carlson, Andrew D
APPLICANT: Huang, Lihua
APPLICANT: Sheliga, Theodore A
TITLE OF INVENTION: Improved Methods for Processing Activated Protein C
FILE REFERENCE: X-11796A
CURRENT APPLICATION NUMBER: US/09/667,570A
CURRENT FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: 60/045,255
PRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patent in version 3.1
SEQ ID NO 3
LENGTH: 419
TYPE: PRT
ORGANISM: Homo sapiens
US-08-667-570A-3

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-442-6672
 TELEFAX: 206-442-6678
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 460 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-756-506-2

Query Match 86.9%; Score 172; DB 2; Length 460;
 Best Local Similarity 75.0%; Fred. No. 5e-21; Indels 0; Gaps 0;
 Matches 33; Conservative 2; Mismatches 9;
 QY 1 ANSFLXLRHSSLEKXCIXXICDFXXAKXIFEDVDDTLAPWSKH 44
 Db 43 ANSFLXLRHSSLEKXCIXXICDFXXAKXIFEDVDDTLAPWSKH 86

Search completed: March 1, 2004, 10:12:20
 Job time: 17.5 secs

(Handwritten signatures and scribbles)

GenCore version 5.1.6
Copyright (C) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2004, 10:01:28 ; Search time 28 Seconds
(without alignments)
331.812 Million cell updates/sec

Title: SEQ1-32GLU-33ASP
Perfect score: 198
Sequence: 1 ANSFLXLRHSLRXCIYX.....XXAKXIFEDVDDTLAFWSKH 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	176	88.9	419	14	US-10-182-263-3
2	176	88.9	419	14	US-10-182-263-4
3	176	88.9	419	14	US-10-182-263-5
4	176	88.9	419	15	US-10-168-407-3
5	176	88.9	419	15	US-10-168-407-4
6	172	86.9	419	14	US-10-298-330-1
7	172	86.9	419	10	US-09-978-917A-4
8	172	86.9	419	14	US-10-182-263-1
9	172	86.9	419	15	US-10-168-407-1
10	172	86.9	461	10	US-09-978-917A-2
11	172	86.9	461	14	US-10-182-263-2
12	172	86.9	461	15	US-10-168-407-2
13	168	84.8	419	14	US-10-182-263-6
14	168	84.8	419	15	US-10-168-407-5
15	168	84.8	419	15	US-10-168-407-6

16	109	55.1	44	14	US-10-298-330-2	Sequence 2, Appli
17	102	51.5	139	15	US-10-360-101-232	Sequence 232, App
18	102	51.5	488	14	US-10-348-504-44	Sequence 44, Appl
19	102	51.5	488	14	US-10-407-123-27	Sequence 27, Appl
20	95	48.0	44	14	US-10-298-330-18	Sequence 18, Appl
21	92	46.5	406	10	US-09-782-587B-3	Sequence 3, Appli
22	92	46.5	406	15	US-10-383-898-1	Sequence 1, Appli
23	92	46.5	466	14	US-10-017-122-2	Sequence 2, Appli
24	92	46.5	466	15	US-10-375-741-14	Sequence 14, Appl
25	91	46.0	42	16	US-10-038-854-97	Sequence 97, Appl
26	89	44.9	44	14	US-10-298-330-3	Sequence 3, Appli
27	89	44.9	406	10	US-09-782-587B-1	Sequence 1, Appli
28	89	44.9	406	14	US-10-109-498-1	Sequence 1, Appli
29	89	44.9	406	14	US-10-255-032-1	Sequence 1, Appli
30	89	44.9	406	14	US-10-281-727-1	Sequence 1, Appli
31	89	44.9	406	15	US-10-386-898-7	Sequence 7, Appli
32	88	44.4	405	15	US-10-360-101-225	Sequence 225, App
33	83	41.9	44	14	US-10-298-330-4	Sequence 4, Appli
34	80	40.4	40	14	US-10-298-330-23	Sequence 23, Appl
35	78	39.4	40	14	US-10-298-330-22	Sequence 22, Appl
36	78	39.4	40	14	US-10-298-330-25	Sequence 25, Appl
37	78	39.4	96	10	US-09-759-130B-313	Sequence 313, App
38	78	39.4	96	14	US-10-189-123-43	Sequence 43, Appl
39	78	39.4	96	14	US-10-188-495-43	Sequence 43, Appl
40	78	39.4	209	10	US-09-759-130B-312	Sequence 312, App
41	78	39.4	209	14	US-10-189-123-42	Sequence 42, Appl
42	78	39.4	209	14	US-10-188-495-42	Sequence 42, Appl
43	78	39.4	226	10	US-09-759-130B-310	Sequence 310, App
44	78	39.4	226	14	US-10-189-123-40	Sequence 40, Appl
45	78	39.4	226	14	US-10-188-495-40	Sequence 40, Appl

ALIGNMENTS

RESULT 1
US-10-182-263-3
; Sequence 3, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/10/182,263
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-3

Query Match 88.9%; Score 176; DB 14; Length 419;
Best Local Similarity 77.3%; Pred. No. 5,6e-21;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 1 ANSFLXLRHSLRXCIYXICDFXXAKXIFEDVDDTLAFWSKH 44
DB 1 ANSFLXLRHSLRXCIYXICDFXXAKXIFEDVDDTLAFWSKH 44

RESULT 2
US-10-182-263-4
; Sequence 4, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:

```
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-4

Query Match      88.9%; Score 176; DB 14; Length 419;
Best Local Similarity 77.3%; Pred. No. 5.6e-21;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANSFLLXLRHSSLRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 ANSFLEELRHGSLERECIEICDFEAKEIFEDVDDTLAFWSKH 44

RESULT 3
US-10-182-263-5
; Sequence 5, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-5

Query Match      88.9%; Score 176; DB 14; Length 419;
Best Local Similarity 77.3%; Pred. No. 5.6e-21;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANSFLLXLRHSSLRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 ANSFLEELRHGSLERECIEICDFEAKEIFEDVDDTLAFWSKH 44

RESULT 4
US-10-168-407-3
; Sequence 3, Application US/10168407
; Publication No. US20030207435A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13610
; CURRENT APPLICATION NUMBER: US/10/168,407
; CURRENT FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 12
```

```
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-407-3

Query Match      88.9%; Score 176; DB 15; Length 419;
Best Local Similarity 77.3%; Pred. No. 5.6e-21;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANSFLLXLRHSSLRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 ANSFLEELRHGSLERECIEICDFEAKEIFEDVDDTLAFWSKH 44

RESULT 5
US-10-168-407-4
; Sequence 4, Application US/10168407
; Publication No. US20030207435A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13610
; CURRENT APPLICATION NUMBER: US/10/168,407
; CURRENT FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-407-4

Query Match      88.9%; Score 176; DB 15; Length 419;
Best Local Similarity 77.3%; Pred. No. 5.6e-21;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANSFLLXLRHSSLRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 ANSFLEELRHGSLERECIEICDFEAKEIFEDVDDTLAFWSKH 44

RESULT 6
US-10-298-330-1
; Sequence 1, Application US/10298330
; Publication No. US20030100506A1
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary L.
; TITLE OF INVENTION: Modified Vitamin K-Dependent
; FILE REFERENCE: 09531-127001
; CURRENT APPLICATION NUMBER: US/10/298,330
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/497,591
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/302,239
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 08/955,636
; PRIOR FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29
; OTHER INFORMATION: Xaa = gamma carboxyglutamic or glutamic acid
US-10-298-330-1
```

US-10-168-407-1
; Sequence 1, Application US/10168407
; Publication No. US20030207435A1

```

/ GENERAL INFORMATION:
/ APPLICANT: Gerlits, Bruce E
/ APPLICANT: Jones, Bryan E
/ APPLICANT: Grinnell, Brian W
/ TITLE OF INVENTION: PROTEIN C
/ FILE REFERENCE: X-13611
/ CURRENT APPLICATION NUMBER: US
/ CURRENT FILING DATE: 2002-07-
/ PRIOR APPLICATION NUMBER: 60/
/ PRIOR FILING DATE: 2002-02-11
/ PRIOR APPLICATION NUMBER: 60/
/ PRIOR FILING DATE: 2000-03-14

```


; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-2

Query Match 86.9%; Score 172; DB 14; Length 461;
Best Local Similarity 75.0%; Pred. No. 2.9e-20;
Matches 33; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

Qy 1 ANSFLLXLRHSSLRXCIXXICDFFXXAKXIFEDVDDTLAFWSKH 44
Db 43 ANSFLEELRQGSLEERCIEICDFFEAKEIFQVDDTLAFWSKH 86

RESULT 12

US-10-168-407-2
; Sequence 2, Application US/10168407
; Publication No. US20030207435A1
; GENERAL INFORMATION:

; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13610
; CURRENT APPLICATION NUMBER: US/10/168,407
; CURRENT FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-407-2

Query Match 86.9%; Score 172; DB 15; Length 461;
Best Local Similarity 75.0%; Pred. No. 2.9e-20;
Matches 33; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

Qy 1 ANSFLLXLRHSSLRXCIXXICDFFXXAKXIFEDVDDTLAFWSKH 44
Db 43 ANSFLEELRQGSLEERCIEICDFFEAKEIFQVDDTLAFWSKH 86

RESULT 13

US-10-182-263-6
; Sequence 6, Application US/10182263
; Publication No. US2003022354A1
; GENERAL INFORMATION:

; APPLICANT: Jones, Bruce E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-07-22
; PRIOR FILING DATE: 2002-02-11
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-6

Query Match 84.8%; Score 168; DB 14; Length 419;
Best Local Similarity 75.0%; Pred. No. 1.2e-19;
Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1 ANSFLLXLRHSSLRXCIXXICDFFXXAKXIFEDVDDTLAFWSKH 44
Db 1 ANSFLEELRQGSLEERCIEICDFFEAKEIFEDVDDTLAFWSKH 44

RESULT 14

US-10-168-407-5
; Sequence 5, Application US/10168407
; Publication No. US20030207435A1
; GENERAL INFORMATION:

; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13610
; CURRENT APPLICATION NUMBER: US/10/168,407
; CURRENT FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-407-5

Query Match 84.8%; Score 168; DB 15; Length 419;
Best Local Similarity 75.0%; Pred. No. 1.2e-19;
Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1 ANSFLLXLRHSSLRXCIXXICDFFXXAKXIFEDVDDTLAFWSKH 44
Db 1 ANSFLEELRQGSLEERCIEICDFFEAKEIFEDVDDTLAFWSKH 44

RESULT 15

US-10-168-407-6
; Sequence 6, Application US/10168407
; Publication No. US20030207435A1
; GENERAL INFORMATION:

; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13610
; CURRENT APPLICATION NUMBER: US/10/168,407
; CURRENT FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-407-6

Query Match 84.8%; Score 168; DB 15; Length 419;
Best Local Similarity 75.0%; Pred. No. 1.2e-19;
Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1 ANSFLLXLRHSSLRXCIXXICDFFXXAKXIFEDVDDTLAFWSKH 44
Db 1 ANSFLEELRQGSLEERCIEICDFFEAKEIFEDVDDTLAFWSKH 44

Search completed: March 1, 2004, 10:11:10
Job time : 30 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2004, 09:54:37 ; Search time 50 Seconds
(without alignments)
248.642 Million cell updates/sec

Title: SEQ1-4SUBS

Perfect score: 197

Sequence: 1 ANSFLXLRGSLRXICIX.....XXAKXIFedVDDTLAFWSKH 44

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	179	90.9	44	2 AAY18300	Modified
2	179	90.9	419	4 AAB82677	Human pro
3	179	90.9	419	4 AAB82678	Human pro
4	179	90.9	419	4 AAE08630	Human pro
5	176	89.3	44	2 AAY18301	Modified
6	174	88.3	419	4 AAB82676	Human pro
7	174	88.3	419	4 AAB82675	Human pro
8	174	88.3	419	4 AAE08628	Human pro
9	174	88.3	419	4 AAE08627	Human pro
10	174	88.3	419	4 AAE08629	Human pro
11	173	87.8	44	2 AAY18298	Modified
12	170	86.3	44	2 AAY18299	Modified
13	168	85.3	44	2 AAY18297	Modified
14	168	85.3	44	2 AAY18307	Modified
15	168	85.3	45	5 ABB79949	Human pro
16	164	83.2	45	5 ABB79946	Human pro
17	164	83.2	45	7 ABB71159	Human pro
18	162	82.2	45	5 ABB79950	Human pro
19	160	81.2	44	2 AAY18309	Modified
20	160	81.2	44	2 AAY18303	Human pro
21	160	81.2	44	4 AAB36402	Human pro
22	160	81.2	44	7 ADD50094	Human vit
23	160	81.2	45	2 AAW5710	Partial h
24	160	81.2	45	5 ABB79947	Human pro
25	160	81.2	45	7 ABB71155	Human pro

26	160	81.2	415	3 AAY56803	Truncated
27	160	81.2	419	2 AAR35760	Protein C
28	160	81.2	419	2 AAW72753	Primary s
29	160	81.2	419	4 AAB82673	Wild-type
30	160	81.2	419	4 AAB36896	Human pro
31	160	81.2	419	4 AAB36897	Human pro
32	160	81.2	419	4 AAB36898	Human pro
33	160	81.2	419	4 AAB36894	Human pro
34	160	81.2	419	4 AAE08625	Human mar
35	160	81.2	419	5 AAU99005	Human pro
36	160	81.2	419	5 AAU99006	Human pro
37	160	81.2	419	5 AAU99008	Human pro
38	160	81.2	419	5 AAU99018	Human pro
39	160	81.2	419	5 AAU99026	Human pro
40	160	81.2	419	5 AAU99037	Human pro
41	160	81.2	419	5 AAU99049	Human pro
42	160	81.2	419	5 AAU99063	Human pro
43	160	81.2	419	5 AAU99072	Human pro
44	160	81.2	419	5 AAU99083	Human pro
45	160	81.2	419	5 AAU99084	Human pro

ALIGNMENTS

RESULT 1
AAY18300
ID AAY18300 standard; peptide; 44 AA.
XX
AC AAY18300;
XX
DT 17-AUG-1999 (first entry)
XX
DE Modified GLA domain of vitamin K-dependent protein.
XX
KW GLA domain; muten; vitamin K-dependent protein; clotting disorder;
XX therapy.
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1..44 /note= "Xaa= gamma-carboxyglutamic acid, or glutamic acid"
FT
XX
PN WC9920767-A1.
XX
PD 29-APR-1999.
XX
PF 20-OCT-1998; 98WO-US022152.
XX
PR 23-OCT-1997; 97US-00955636.
XX (MINU) UNIV MINNESOTA.
XX Nelsestuen GL;
XX
DR WPI; 1999-288309/24.
XX
PT Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain, useful for treating clotting disorders.
XX
PS Claim 9; Page 79; 86pp; English.
XX
CC This sequence represents a modified GLA (gamma-carboxyglutamic acid) domain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances membrane binding of the modified polypeptide as compared to the native polypeptide. The polypeptide is used to treat a clotting disorder by decreasing or increasing clot formation. Modification of the GLA domain results in a protein which has enhanced membrane binding affinity as compared to the native protein

```
XX SQ Sequence 44 AA;
Query Match 90.9%; Score 179; DB 2; Length 44;
Best Local Similarity 100.0%; Pred. No. 2.3e-22;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANSFLXXLRQGSIXRXCIXXICDPFXAKXIFEDVDDTLAFWSKH 44
Db 1 ANSFLXXLRQGSIXRXCIXXICDPFXAKXIFEDVDDTLAFWSKH 44

RESULT 2
AAB82677
ID AAB82677 standard; protein; 419 AA.
XX AC AAB82677;
XX DT 15-OCT-2001 (first entry)
XX DE Human protein C derivative (H10Q/S11G/Q32E/N33D/L194S).
XX KW Protein C; human; coronary syndrome; thrombosis; angina;
XX KW myocardial infarction; vascular occlusive disorder; hypercoagulation;
XX KW sepsis; protein C deficiency; occlusion; thromboembolism; stenosis;
XX KW antibacterial; immunosuppressive; thrombolytic; cordiant; antianginal;
XX KW anticoagulant; therapy; mutant; mutuin.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Location/Qualifiers
FT Domain 1..45 /note= "Gla domain"
FT Modified-site 6 /note= "gamma-carboxylated"
FT Modified-site 7 /note= "gamma-carboxylated"
FT Misc-difference 10 /note= "gamma-carboxylated"
FT Misc-difference 11 /note= "His in wild-type protein"
FT Modified-site 14 /note= "Ser in wild-type protein"
FT Modified-site 16 /note= "gamma-carboxylated"
FT Modified-site 19 /note= "gamma-carboxylated"
FT Modified-site 20 /note= "gamma-carboxylated"
FT Modified-site 25 /note= "gamma-carboxylated"
FT Modified-site 26 /note= "gamma-carboxylated"
FT Modified-site 29 /note= "gamma-carboxylated"
FT Misc-difference 32 /note= "N-glycosylated"
FT Misc-difference 33 /note= "Gln in wild-type protein"
FT Disulfide-bond 50..69 /note= "Asn in wild-type protein"
FT Disulfide-bond 59..64
FT Disulfide-bond 80..89
FT Disulfide-bond 98..109
FT Disulfide-bond 120..133
FT Disulfide-bond 141..277
FT Cleavage-site 156..157
FT /note= "cleavage makes a 2-chain inactive precursor (155-
FT amino acid light chain attached via a disulfide bond to a
FT 262-amino acid heavy chain)"
FT Peptide 158..169
FT /note= "activation peptide; removal activates the 2-chain
FT zymogen"
```

```
FT Cleavage-site 169..170
FT /note= "thrombin cleavage site"
FT Misc-difference 194
FT Disulfide-bond /note= "Leu in wild-type protein"
FT Modified-site 248 /note= "N-glycosylated"
FT Modified-site 313 /note= "N-glycosylated"
FT Modified-site 329 /note= "N-glycosylated"
FT Disulfide-bond 331..345
FT Disulfide-bond 356..384
XX WO200157193-A2.
XX PV 09-AUG-2001.
XX PD 19-JAN-2001; 2001WO-US0000020.
XX PF 02-FEB-2000; 2000US-0179801P.
XX PR 14-MAR-2000; 2000US-0189197P.
XX PA (EJIL ) LILLY & CO ELI.
XX PI Gerlitz BE, Jones BE;
XX DR WPI; 2001-496919/54.
XX DR N-PSDB; AAB26365.
XX PT Novel human protein C derivative for treating, e.g., myocardial
FT infarction, unstable angina, sepsis, thrombotic disorders, acute arterial
FT thrombotic occlusion, and thromboembolism.
XX PS Claim 5; Page 54-55; 63pp; English.
XX CC The present sequence is that of a claimed human protein C derivative in
CC which His at position 10 of the mature wild-type protein C sequence (see
CC AAB82673) is substituted with Gln, Ser at position 11 with Gly, Gln at
CC position 32 with Glu, Asn at position 33 with Asp, and Leu at position
CC 194 with Ser. It is an example of protein C derivatives of the invention
CC that have at least 2 amino acid substitutions, but which have increased
CC anticoagulant activity and resistance to inactivation by serpins compared
CC with the wild-type protein, while retaining the biological activity of
CC the wild-type protein. A method of producing the derivatives using
CC recombinant DNA methods is claimed. The protein C derivatives are useful
CC for treating coronary syndromes and disease states predisposing to
CC thrombosis (e.g. myocardial infarction and unstable angina), vascular
CC occlusive disorders and hypercoagulable states, sepsis (in combination
CC with bactericidal permeability increasing protein or with tissue factor
CC pathway inhibitor) thrombotic disorders (in combination with an anti-
CC platelet agent or by local delivery through an intracoronary catheter),
CC protein C deficiency, acute arterial thrombotic occlusion,
CC thromboembolism, or stenosis in coronary, cerebral or peripheral arteries
CC or in vascular grafts. Human patients with genetically predisposed
CC prothrombotic disorders may be treated by gene therapy (all claimed)
XX SQ Sequence 419 AA;
```

```
Query Match 90.9%; Score 179; DB 4; Length 419;
Best Local Similarity 79.5%; Pred. No. 2.5e-21;
Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 ANSFLXXLRQGSIXRXCIXXICDPFXAKXIFEDVDDTLAFWSKH 44
Db 1 ANSFLXXLRQGSIXRXCIXXICDPFXAKXIFEDVDDTLAFWSKH 44

RESULT 3
AAB82678
ID AAB82678 standard; protein; 419 AA.
XX AC AAB82678;
```

XX 15-OCT-2001 (first entry)
 XX Human protein C derivative (H10Q/S11G/Q32E/N33D/L194S/T254S).
 DE Protein C; human; coronary syndrome; thrombosis; angina;
 XX myocardial infarction; vascular occlusive disorder; hypercoagulation;
 KW sepsis; protein C deficiency; occlusion; thromboembolism; stenosis;
 KW antibacterial; immunosuppressive; thrombolytic; cardiac; antianginal;
 KW anticoagulant; therapy; mutant; mutein.
 XX Homo sapiens.
 OS Synthetic.
 XX Key Location/Qualifiers
 FT Domain 1..45
 FT /note= "Gla domain"
 FT Modified-site 6
 FT /note= "gamma-carboxylated"
 FT Modified-site 7
 FT /note= "gamma-carboxylated"
 FT Misc-difference 10
 FT /note= "gamma-carboxylated"
 FT Misc-difference 11
 FT /note= "His in wild-type protein"
 FT Modified-site 14
 FT /note= "Ser in wild-type protein"
 FT Modified-site 16
 FT /note= "gamma-carboxylated"
 FT Modified-site 19
 FT /note= "gamma-carboxylated"
 FT Modified-site 20
 FT /note= "gamma-carboxylated"
 FT Modified-site 25
 FT /note= "gamma-carboxylated"
 FT Modified-site 26
 FT /note= "gamma-carboxylated"
 FT Modified-site 29
 FT /note= "N-glycosylated"
 FT Misc-difference 32
 FT /note= "Gln in wild-type protein"
 FT Misc-difference 33
 FT /note= "Asn in wild-type protein"
 FT Disulfide-bond 50..69
 FT Disulfide-bond 59..64
 FT Disulfide-bond 80..89
 FT Disulfide-bond 98..109
 FT Disulfide-bond 120..133
 FT Disulfide-bond 141..277
 FT Cleavage-site 156..157
 FT /note= "cleavage makes a 2-chain inactive precursor (155-
 FT amino acid light chain attached via a disulfide bond to a
 FT 262-amino acid heavy chain)"
 FT Peptide 158..169
 FT /note= "activation peptide; removal activates the 2-chain
 FT zymogen"
 FT Cleavage-site 169..170
 FT /note= "thrombin cleavage site"
 FT Misc-difference 194
 FT /note= "Leu in wild-type protein"
 FT Disulfide-bond 196..212
 FT Modified-site 248
 FT /note= "N-glycosylated"
 FT Misc-difference 254
 FT /note= "Thr in wild-type protein"
 FT Modified-site 313
 FT /note= "N-glycosylated"
 FT Modified-site 329
 FT /note= "N-glycosylated"
 FT Disulfide-bond 331..345
 FT Disulfide-bond 356..384
 XX WO200157193-A2.

XX 09-AUG-2001.
 XX 19-JAN-2001; 2001WO-US000020.
 XX 02-FEB-2000; 2000US-0179801P.
 PR 14-MAR-2000; 2000US-0189197P.
 XX (BLIL) LILLY & CO ELI.
 XX Gerlitz BE, Jones BE;
 XX WPI; 2001-496919/54.
 XX Novel human protein C derivative for treating, e.g., myocardial
 FT infarction, unstable angina, sepsis, thrombotic disorders, acute arterial
 FT thrombotic occlusion, and thromboembolism.
 XX Claim 6; Page 56-57; 63pp; English.
 XX The present sequence is that of a claimed human protein C derivative in
 CC which His at position 10 of the wild-type protein C sequence (see
 CC AAB82673) is substituted with Gln, Ser at position 11 with Gly, Gln at
 CC position 32 with Glu, Asn at position 33 with Asp, Leu at position 194
 CC with Ser, and Thr at position 254 with Ser. It is an example of protein C
 CC derivatives of the invention that have at least 2 amino acid
 CC substitutions, but which have increased anticoagulant activity and
 CC resistance to inactivation by serpins compared with the wild-type
 CC protein, while retaining the biological activity of the wild-type
 CC protein. A method of producing the derivatives using recombinant DNA
 CC methods is claimed. The protein C derivatives are useful for treating
 CC coronary syndromes and disease states predisposing to thrombosis (e.g.
 CC myocardial infarction and unstable angina), vascular occlusive disorders
 CC and hypercoagulable states, sepsis (in combination with bactericidal
 CC permeability increasing protein or with tissue factor pathway inhibitor),
 CC thrombotic disorders (in combination with an anti-platelet agent or by
 CC local delivery through an intracoronary catheter), protein C deficiency,
 CC acute arterial thrombotic occlusion, thromboembolism, or stenosis in
 CC coronary; cerebral or peripheral arteries or in vascular grafts. Human
 CC patients with genetically predisposed prothrombotic disorders may be
 CC treated by gene therapy (all claimed)
 XX Sequence 419 AA;
 SQ
 Query Match 90.9%; Score 179; DB 4; Length 419;
 Best Local Similarity 79.5%; Pred. No. 2.5e-21;
 Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 1 ANSFLXLRQGSLSRXCIXXICDFXAXKXIFEDVDVDTLAFWSKH 44
 DB 1 ANSFLXLRQGSLSRXCIXXICDFXAXKXIFEDVDVDTLAFWSKH 44
 RESULT 4
 ID AAE08630 standard; protein; 419 AA.
 XX AAE08630;
 AC AAE08630;
 DT 01-NOV-2001 (first entry)
 XX Human protein C derivative #4.
 KW Human; protein C derivative; anticoagulation activity; thrombosis;
 KW serpin inactivation; acute coronary syndrome; myocardial infarction;
 KW vascular occlusive disorder; hypercoagulable state; angina; sepsis;
 KW disseminated intravascular coagulation; DIC; burn; transplantation;
 KW sickle cell disease; viral haemorrhagic fever; protein C deficiency;
 KW haemolytic uremic syndrome; acute arterial thrombotic occlusion;
 KW thromboembolism; prothrombotic disorder; gene therapy; thalassaemia.
 XX Homo sapiens.
 OS XX

FN WO200159084-A1.
 XX 16-AUG-2001.
 PD 02-FEB-2001; 2001WO-US001221.
 PF 11-FEB-2000; 2000US-0181948P.
 PR 14-MAR-2000; 2000US-0189199P.
 XX (ELIL) LILLY & CO ELI.
 PA Gerlitz BE, Grinnell BW, Jones BE,
 XX WPI; 2001-5146G2/56.
 PI N-PSDB; AAD15228.
 DR Protein C derivative for treating acute coronary syndromes, vascular
 XX occlusive disorders, thrombotic disorders and sepsis, comprises
 PT substitutions at specified amino acid positions.
 FT
 PS Claim 6; Page 50-51; 59pp; English.
 XX This invention relates to human protein C derivatives and nucleic acid
 CC molecules encoding such derivatives. These derivatives have increased
 CC anticoagulation activity, resistance to serpin inactivation and increased
 CC sensitivity to thrombin activation compared to wild type protein C, and
 CC retains the biological activity of the wild type human protein C. Protein
 CC C derivatives are useful in the manufacture of a medicament for the
 CC treatment of acute coronary syndromes e.g. myocardial infarction and
 CC unstable angina; and disease states predisposing to thrombosis; vascular
 CC intravascular coagulation (DIC), burns, transplantations, thalassaemia,
 CC sickle cell disease, viral haemorrhagic fever and haemolytic uremic
 CC syndrome; sepsis in combination with bacterial permeability increasing
 CC protein; thrombotic disorders in combination with an anti-platelet agent;
 CC protein C deficiency; acute arterial thrombotic occlusion,
 CC thromboembolism or stenosis in coronary, cerebral or peripheral arteries
 CC or in vascular grafts in combination with a thrombolytic agent. Nucleic
 CC acid molecules of the invention are useful for treating humans with
 CC genetically predisposed prothrombotic disorders by gene therapy. The
 CC present sequence is human protein C derivative
 XX
 SQ Sequence 419 AA;
 Query Match 90.9%; Score 179; DB 4; Length 419;
 Best Local Similarity 79.5%; Pred. No. 2.5e-21;
 Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 1 ANSFLXXLRQGSIXXCIXXICDFXXAKXIFEDVDTLAFWSKH 44
 DB 1 ANSFLXXLRQGSIXXCIXXICDFEEAKXIFEDVDTLAFWSKH 44
 RESULT 5
 AAY18301
 ID AAY18301 standard; peptide; 44 AA.
 AC AAY18301;
 XX 17-AUG-1999 (first entry)
 DT Modified GLA domain of vitamin K-dependent protein.
 DE GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
 XX therapy.
 KW Homo sapiens.
 XX Synthetic.
 OS Key Location/Qualifiers
 FT Misc-difference 1..44
 FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic
 FT acid"

XX WO9920767-A1.
 FN 29-APR-1999.
 PD 20-OCT-1998; 98WO-US022152.
 PF 23-OCT-1997; 97US-00955636.
 PR (MINU) UNIV MINNESOTA.
 XX Neisestuen GL;
 XX WPI; 1999-288309/24.
 DR Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid
 XX domain, useful for treating clotting disorders.
 FT
 PS Claim 9; Page 82; 86pp; English.
 XX This sequence represents a modified GLA (gamma-carboxyglutamic acid)
 CC domain. The invention relates to a vitamin K-dependent polypeptide
 CC comprising a modified GLA domain containing an amino acid substitution
 CC which enhances membrane binding of the modified polypeptide as compared
 CC to the native polypeptide. The polypeptide is used to treat a clotting
 CC disorder by decreasing or increasing clot formation. Modification of the
 CC GLA domain results in a protein which has enhanced membrane binding
 CC affinity as compared to the native protein
 XX
 SQ Sequence 44 AA;
 Query Match 89.3%; Score 176; DB 2; Length 44;
 Best Local Similarity 97.7%; Pred. No. 7.2e-22;
 Matches 43; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ANSFLXXLRQGSIXXCIXXICDFXXAKXIFEDVDTLAFWSKH 44
 DB 1 ANSFLXXLRQGSIXXCIXXICDFXXAKXIFEDVDTLAFWSKH 44
 RESULT 6
 AAB82676
 ID AAB82676 standard; protein; 419 AA.
 AC AAB82676;
 XX 15-OCT-2001 (first entry)
 DT Human protein C derivative (S11G/Q32E/N33D/L194S/T254S).
 DE Protein C; human; coronary syndrome; thrombosis; angina;
 KW myocardial infarction; vascular occlusive disorder; hypercoagulation;
 KW sepsis; protein C deficiency; occlusion; thromboembolism; stenosis;
 KW antibacterial; immunosuppressive; thrombolytic; cardiant; antianginal;
 KW anticoagulant; therapy; mutant; mutein.
 XX Homo sapiens.
 OS Synthetic.
 XX Key Location/Qualifiers
 FT Domain 1..45
 FT /note= "GLA domain"
 FT Modified-site 6
 FT /note= "gamma-carboxylated"
 FT Modified-site 7
 FT /note= "gamma-carboxylated"
 FT Misc-difference 11
 FT /note= "Ser in wild-type protein"
 FT Modified-site 14
 FT /note= "gamma-carboxylated"
 FT Modified-site 16
 FT /note= "gamma-carboxylated"
 FT Modified-site 19

FT Disulfide-bond 120..133
 FT Disulfide-bond 141..277
 FT Cleavage-site 156..157
 /note= "cleavage makes a 2-chain inactive precursor (155-
 FT amino acid light chain attached via a disulfide bond to a
 FT 262-amino acid heavy chain)"
 FT Peptide 158..169
 /note= "activation peptide; removal activates the 2-chain
 FT zymogen"
 FT Cleavage-site 169..170
 /note= "thrombin cleavage site"
 FT Misc-difference 194
 /note= "Leu in wild-type protein"
 FT Disulfide-bond 196..212
 FT Modified-site 248
 /note= "N-glycosylated"
 FT Modified-site 313
 /note= "N-glycosylated"
 FT Modified-site 329
 /note= "N-glycosylated"
 FT Disulfide-bond 331..345
 FT Disulfide-bond 356..384
 WO200157193-A2.
 PN
 XX
 XX
 PD 09-AUG-2001.
 XX
 XX 19-JAN-2001; 2001WO-US000020.
 XX
 XX 02-FEB-2000; 2000US-0179801P.
 PR 14-MAR-2000; 2000US-0189197P.
 PR
 XX (ELIL) LILLY & CO ELI.
 PA
 XX Gerlitz BE, Jones BE;
 PI
 XX WPI; 2001-496919/54.
 DR N-PSDB; AAH26363.
 XX
 XX Novel human protein C derivative for treating, e.g., myocardial
 PT infarction, unstable angina, sepsis, thrombotic disorders, acute arterial
 PT thrombotic occlusion, and thromboembolism.
 PS
 XX Claim 3; Page 52-53; 63pp; English.
 XX
 CC The present sequence is that of a claimed human protein C derivative in
 CC which Ser at amino acid position 11 of the mature wild-type protein C
 CC sequence (see AAB82673) is substituted with Gly, Gln at position 32 with
 CC Glu, Asn at position 33 with Asp, and Leu at position 194 with Ser. The
 CC protein is an example of protein C derivatives of the invention that have
 CC at least 2 amino acid substitutions, but which have increased
 CC anticoagulant activity and resistance to inactivation by serpins compared
 CC with the wild-type protein, while retaining the biological activity of
 CC the wild-type protein. A method of producing the derivatives using
 CC recombinant DNA methods is claimed. The protein C derivatives are useful
 CC for treating coronary syndromes and disease states predisposing to
 CC thrombosis (e.g. myocardial infarction and unstable angina), vascular
 CC occlusive disorders and hypercoagulable states, sepsis (in combination
 CC with bactericidal permeability increasing protein or with tissue factor
 CC pathway inhibitor), thrombotic disorders (in combination with an anti-
 CC platelet agent or by local delivery through an intracoronary catheter),
 CC Protein C deficiency, acute arterial thrombotic occlusion,
 CC thromboembolism, or stenosis in coronary, cerebral or peripheral arteries
 CC or in vascular grafts. Human patients with genetically predisposed
 CC prothrombotic disorders may be treated by gene therapy (all claimed)
 XX
 XX Sequence 419 AA;

Query Match 88.3%; Score 174; DB 4; Length 419;
 Best Local Similarity 77.3%; Pred. No. 1.7e-20;
 Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 1 ANSFLXLRQGSLLRXRCIXXICDFXXAKXIFEDVDDTLAFWSKH 44

Db 1 ANSFLXLRHGSLSRECIIEICDFEAKKEIFEDVDDTLAFWSKH 44
 RESULT 8
 AAE08628
 ID AAE08628 standard; protein; 419 AA.
 XX
 AC AAE08628;
 XX
 DT 01-NOV-2001 (first entry)
 XX
 DE Human protein C derivative #2.
 XX
 KW Human; protein C derivative; anticoagulation activity; thrombosis;
 KW serpin inactivation; acute coronary syndrome; myocardial infarction;
 KW vascular occlusive disorder; hypercoagulable state; angina; sepsis;
 KW disseminated intravascular coagulation; DIC; burn; transplantation;
 KW sickle cell disease; viral haemorrhagic fever; protein C deficiency;
 KW haemolytic uraemic syndrome; acute arterial thrombotic occlusion;
 KW thromboembolism; prothrombotic disorder; gene therapy; thalassaemia.
 XX
 OS Homo sapiens.
 XX
 XX WO200159084-A1.
 XX
 XX 16-AUG-2001.
 XX
 XX 02-FEB-2001; 2001WO-US001221.
 PF
 XX 11-FEB-2000; 2000US-0181948P.
 PR 14-MAR-2000; 2000US-0189199P.
 PR
 XX (ELIL) LILLY & CO ELI.
 PA
 XX Gerlitz BE, Grinnell BW, Jones BE;
 PI
 XX WPI; 2001-514662/56.
 DR N-PSDB; AAD15226.
 XX
 XX Protein C derivative for treating acute coronary syndromes, vascular
 PT occlusive disorders, thrombotic disorders and sepsis, comprises
 PT substitutions at specified amino acid positions.
 PS
 XX Claim 4; Page 47-48; 59pp; English.
 XX
 CC The invention relates to human protein C derivatives and nucleic acid
 CC molecules encoding such derivatives. These derivatives have increased
 CC anticoagulation activity, resistance to serpin inactivation and increased
 CC sensitivity to thrombin activation compared to wild type protein C, and
 CC retains the biological activity of the wild type human protein C. Protein
 CC C derivatives are useful in the manufacture of a medicament for the
 CC treatment of acute coronary syndromes e.g. myocardial infarction and
 CC unstable angina; and disease states predisposing to thrombosis; vascular
 CC occlusive disorders and hypercoagulable states e.g. disseminated
 CC intravascular coagulation (DIC), burns, transplantations, thalassaemia,
 CC sickle cell disease, viral haemorrhagic fever and haemolytic uraemic
 CC syndrome; sepsis in combination with bacterial permeability increasing
 CC protein; thrombotic disorders in combination with an anti-platelet agent;
 CC protein C deficiency; acute arterial thrombotic occlusion,
 CC thromboembolism or stenosis in coronary, cerebral or peripheral arteries
 CC or in vascular grafts in combination with a thrombolytic agent. Nucleic
 CC acid molecules of the invention are useful for treating humans with.
 CC genetically predisposed prothrombotic disorders by gene therapy. The
 CC present sequence is human protein C derivative
 XX
 XX Sequence 419 AA;

Query Match 88.3%; Score 174; DB 4; Length 419;
 Best Local Similarity 77.3%; Pred. No. 1.7e-20;
 Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 1 ANSFLXLRQGSLLRXRCIXXICDFXXAKXIFEDVDDTLAFWSKH 44

DB 1 ANSFLEELRSGSLERECIEICDFEAKEIFEDVDDTLAFWSKH 44

RESULT 9
AAE08627
ID AAE08627 standard; protein; 419 AA.
XX AC AAE08627;
XX DT 01-NOV-2001 (first entry)
XX DE Human protein C derivative #1.
XX KW Human; protein C derivative; anticoagulation activity; thrombosis;
KW serpin inactivation; acute coronary syndrome; myocardial infarction;
KW vascular occlusive disorder; hypercoagulable state; angina; sepsis;
KW disseminated intravascular coagulation; DIC; burn; transplantation;
KW sickle cell disease; viral haemorrhagic fever; protein C deficiency;
KW haemolytic uremic syndrome; acute arterial thrombotic occlusion;
KW thromboembolism; prothrombotic disorder; gene therapy; thalassaemia.
XX OS Homo sapiens.
XX PN WO200159084-A1.
XX PD 16-AUG-2001.
XX PF 02-FEB-2001; 2001WO-US001221.
XX PR 11-FEB-2000; 2000US-0181948P.
XX PR 14-MAR-2000; 2000US-0189199P.
XX PA (ELIL) LILLY & CO ELI.
XX PI Gerlitz BE, Grinnell BW, Jones BE;
XX WPI; 2001-514562/56.
XX DR N-PSDB; AAD15225.
XX PT Protein C derivative for treating acute coronary syndromes, vascular
XX occlusive disorders, thrombotic disorders and sepsis, comprises
XX substitutions at specified amino acid positions.
XX PS Claim 3; Page 46-47; 59pp; English.
XX CC The invention relates to human protein C derivatives and nucleic acid
XX molecules encoding such derivatives. These derivatives have increased
XX anticoagulation activity, resistance to serpin inactivation and increased
XX sensitivity to thrombin activation compared to wild type protein C, and
XX retains the biological activity of the wild type human protein C. Protein
XX C derivatives are useful in the manufacture of a medicament for the
XX treatment of acute coronary syndromes e.g. myocardial infarction and
XX unstable angina; and disease states predisposing to thrombosis; vascular
XX occlusive disorders and hypercoagulable states e.g. disseminated
XX intravascular coagulation (DIC), burns, transplantations, thalassaemia,
XX sickle cell disease, viral haemorrhagic fever and haemolytic uremic
XX syndrome; sepsis in combination with bacterial permeability increasing
XX protein; thrombotic disorders in combination with an anti-platelet agent;
XX protein C deficiency; acute arterial thrombotic occlusion;
XX thromboembolism or stenosis in coronary, cerebral or peripheral arteries
XX or in vascular grafts in combination with a thrombolytic agent. Nucleic
XX acid molecules of the invention are useful for treating humans with
XX genetically predisposed prothrombotic disorders by gene therapy. The
XX present sequence is human protein C derivative
XX Sequence 419 AA;

Query Match 88.3%; Score 174; DB 4; Length 419;
Best Local Similarity 77.3%; Pred. No. 1.7e-20;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 1 ANSFLEXLRQSLRXCIXXICDFEAKEIFEDVDDTLAFWSKH 44

DB 1 ANSFLEELRSGSLERECIEICDFEAKEIFEDVDDTLAFWSKH 44

RESULT 10
AAE08629
ID AAE08629 standard; protein; 419 AA.
XX AC AAE08629;
XX DT 01-NOV-2001 (first entry)
XX DE Human protein C derivative #3.
XX KW Human; protein C derivative; anticoagulation activity; thrombosis;
KW serpin inactivation; acute coronary syndrome; myocardial infarction;
KW vascular occlusive disorder; hypercoagulable state; angina; sepsis;
KW disseminated intravascular coagulation; DIC; burn; transplantation;
KW sickle cell disease; viral haemorrhagic fever; protein C deficiency;
KW haemolytic uremic syndrome; acute arterial thrombotic occlusion;
KW thromboembolism; prothrombotic disorder; gene therapy; thalassaemia.
XX OS Homo sapiens.
XX PN WO200159084-A1.
XX PD 16-AUG-2001.
XX PF 02-FEB-2001; 2001WO-US001221.
XX PR 11-FEB-2000; 2000US-0181948P.
XX PR 14-MAR-2000; 2000US-0189199P.
XX PA (ELIL) LILLY & CO ELI.
XX PI Gerlitz BE, Grinnell BW, Jones BE;
XX WPI; 2001-514662/56.
XX DR N-PSDB; AAD15227.
XX PT Protein C derivative for treating acute coronary syndromes, vascular
XX occlusive disorders, thrombotic disorders and sepsis, comprises
XX substitutions at specified amino acid positions.
XX PS Claim 5; Page 48-49; 59pp; English.
XX CC The invention relates to human protein C derivatives and nucleic acid
XX molecules encoding such derivatives. These derivatives have increased
XX anticoagulation activity, resistance to serpin inactivation and increased
XX sensitivity to thrombin activation compared to wild type protein C, and
XX retains the biological activity of the wild type human protein C. Protein
XX C derivatives are useful in the manufacture of a medicament for the
XX treatment of acute coronary syndromes e.g. myocardial infarction and
XX unstable angina; and disease states predisposing to thrombosis; vascular
XX occlusive disorders and hypercoagulable states e.g. disseminated
XX intravascular coagulation (DIC), burns, transplantations, thalassaemia,
XX sickle cell disease, viral haemorrhagic fever and haemolytic uremic
XX syndrome; sepsis in combination with bacterial permeability increasing
XX protein; thrombotic disorders in combination with an anti-platelet agent;
XX protein C deficiency; acute arterial thrombotic occlusion;
XX thromboembolism or stenosis in coronary, cerebral or peripheral arteries
XX or in vascular grafts in combination with a thrombolytic agent. Nucleic
XX acid molecules of the invention are useful for treating humans with
XX genetically predisposed prothrombotic disorders by gene therapy. The
XX present sequence is human protein C derivative
XX Sequence 419 AA;

Query Match 88.3%; Score 174; DB 4; Length 419;

XX	17-AUG-1999	(first entry)
DT		
XX	Modified GLA domain of vitamin K-dependent protein.	
DE		
XX	GLA domain; mutein; vitamin K-dependent protein; clotting disorder;	
KW	therapy.	
XX		
XX	Homo sapiens.	
OS	Synthetic.	
XX		
XX	Key	Location/Qualifiers
PH		
FT	Misc-difference 1. .44	
FT	/note= "Xaa= gamma-carboxyglutamic acid, or glutamic	
FT	acid"	
XX		
XX	WO920767-A1.	
PN		
XX		
XX	29-APR-1999.	
PD		
XX		
XX	20-OCT-1998; 98WO-US022152.	
PF		
XX		
XX	23-OCT-1997; 97US-00955636.	
PR		
XX		
XX	(MINU) UNIV MINNESOTA.	
PA		
XX		
XX	Nelsestuen GL;	
PI		
XX		
XX	WPI; 1999-288309/24.	
DR		
XX		
XX	Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid	
PT	domain, useful for treating clotting disorders.	
PT		
PT		
XX		
XX	Claim 8; Page 78; 86pp; English.	
PS		
XX		
CC	This sequence represents a modified GLA (gamma-carboxyglutamic acid)	
CC	domain. The invention relates to a vitamin K-dependent polypeptide	
CC	comprising a modified GLA domain containing an amino acid substitution	
CC	which enhances membrane binding of the modified polypeptide as compared	
CC	to the native polypeptide. The polypeptide is used to treat a clotting	
CC	disorder by decreasing or increasing clot formation. Modification of the	
CC	GLA domain results in a protein which has enhanced membrane binding	
CC	affinity as compared to the native protein	
XX		
SQ	Sequence 44 AA;	
	Query Match 86.3%; Score 170; DB 2; Length 44;	
	Best Local Similarity 95.5%; Pred. No. 7.4e-21;	
	Matches 42; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
QY	1 ANSFLXLRQSLRXCIXCXICDFXXAKXIFEDVDDTLAFWSKH 44	
	: : : : : : :	
Db	1 ANSFLXLRRESSLXRCIXCXICDFXXAKXIFEDVDDTLAFWSKH 44	
	: : : : : : :	
RESULT 13		
AAV18297		
ID	AAV18297 standard; pep:ide; 44 AA.	
XX		
XX	AAV18297;	
XX		
DT	17-AUG-1999 (first entry)	
XX		
XX	Modified GLA domain of vitamin K-dependent protein.	
DE		
XX	GLA domain; mutein; vitamin K-dependent protein; clotting disorder;	
KW	therapy.	
XX		
XX	Homo sapiens.	
OS	Synthetic.	
XX		
XX	Key	Location/Qualifiers
PH		
FT	Misc-difference 1. .44	
FT		

FT FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic
XX XX acid"
PN WO9920767-A1.
XX
XX
PD 29-APR-1999.
XX
XX PF 20-OCT-1998; 98WO-US022152.
XX PR 23-OCT-1997; 97US-00955636.
XX (MINU) UNIV MINNESOTA.
XX Nelsestuen GL;
XX
XX WPI; 1999-288309/24.
XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid
PT domain, useful for treating clotting disorders.
XX
XX Claim 6; Page 78; 86pp; English.
XX
XX This sequence represents a modified GLA (gamma-carboxyglutamic acid)
CC domain. The invention relates to a vitamin K-dependent polypeptide
CC comprising a modified GLA domain containing an amino acid substitution
CC which enhances membrane binding of the modified polypeptide as compared
CC to the native polypeptide. The polypeptide is used to treat a clotting
CC disorder by decreasing or increasing clot formation. Modification of the
CC GLA domain results in a protein which has enhanced membrane binding
CC affinity as compared to the native protein
XX
XX Sequence 44 AA;
SQ

Query Match 85.3%; Score 168; DB 2; Length 44;
Best Local Similarity 95.5%; Pred. No. 1.6e-20;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 ANSFLXLRQSLRXCIIXICDFXXAKXIFEDVDDTLAFWSKH 44
Db 1 ANSFLXLRHSSLRXCIIXICDFXXAKXIFEDVDDTLAFWSKH 44

RESULT 14
AAY18307
ID AAY18307 standard; peptide; 44 AA.
XX
XX AAY18307;
AC
XX
XX 17-AUG-1999 (first entry)
DT
XX
XX Modified GLA domain of vitamin K-dependent protein.
DE
XX
XX GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
KW therapy.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 1...44
FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic
FT acid"
FT
XX WO9920767-A1.
PN
XX
XX 29-APR-1999.
PD
XX
XX 20-OCT-1998; 98WO-US022152.
PF
XX 23-OCT-1997; 97US-00955636.
PR (MINU) UNIV MINNESOTA.
PA
XX

PI Nelsestuen GL;
XX
XX WPI; 1999-288309/24.
XX
XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid
PT domain, useful for treating clotting disorders.
XX
XX Disclosure; Page 79; 86pp; English.
XX
XX This sequence represents a modified GLA (gamma-carboxyglutamic acid)
CC domain. The invention relates to a vitamin K-dependent polypeptide
CC comprising a modified GLA domain containing an amino acid substitution
CC which enhances membrane binding of the modified polypeptide as compared
CC to the native polypeptide. The polypeptide is used to treat a clotting
CC disorder by decreasing or increasing clot formation. Modification of the
CC GLA domain results in a protein which has enhanced membrane binding
CC affinity as compared to the native protein
XX
XX Sequence 44 AA;
SQ

Query Match 85.3%; Score 168; DB 2; Length 44;
Best Local Similarity 95.5%; Pred. No. 1.6e-20;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 ANSFLXLRQSLRXCIIXICDFXXAKXIFEDVDDTLAFWSKH 44
Db 1 ANSFLXLRDSSLRXCIIXICDFXXAKXIFEDVDDTLAFWSKH 44

RESULT 15
ABB79949
ID ABB79949 standard; protein; 45 AA.
XX
XX ABB79949;
AC
XX
XX 12-DEC-2002 (first entry)
DT
XX
XX Human protein C mutated Gla domain QGN.
DE
XX
XX Protein C; Gla domain; human; blood clotting; anticoagulant;
KW thrombolytic; antiarteriosclerotic; cardiant; antiaggregant; mutant;
KW muten.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 10
FT /note= "wild-type His substituted by Gln"
FT
FT Misc-difference 11 /note= "wild-type Ser substituted by Gly"
FT Misc-difference 12 /note= "wild-type Ser substituted by Gln"
XX
XX WO200270681-A1.
PN
XX
XX 12-SEP-2002.
PD
XX
XX 01-MAR-2002; 2002WO-SE000363.
PF
XX
XX 02-MAR-2001; 2001US-0272466P.
PR (TACT-) TAC THROMBOSIS & COAGULATION AB.
XX
XX Dahlbaeck B;
PI
XX
XX WPI; 2002-713449/77.
XX
XX New variant blood coagulation component, useful for manufacturing a
XX PT medicament for treating or preventing coagulation disorders, e.g.
XX PT thrombosis, comprises an anticoagulant activity in the protein C-
XX PT anticoagulant system of blood.
XX

PS Example 1; Page; 50pp; English.

XX The present sequence is the protein sequence of a mutated Gla domain (N-
CC terminal amino acids 1-45) of human protein C. The mutated Gla domain
CC contains the substitution mutations H10Q, S11G and S12N. Protein C and
CC activated protein C variants comprising a mutated Gla domain are provided
CC by the invention. The variants contain at least 5, and optionally 7-10,
CC amino acid substitutions. A preferred mutant (designated QGNSEEDY, see
CC ABB79946) has the mutations H10Q, S11G, S12N, D23S, Q32E, N33D and H44Y,
CC and shows greatly enhanced anticoagulant activity in standard in vitro
CC coagulation assays. The present mutant (designated QGN) was produced in
CC an example from the invention as a step toward the production of the
CC QGNSEEDY mutant Gla domain, and shows little, if any, improvement in
CC anticoagulant activity over wild-type activated protein C. The invention
CC provides methods for producing the variants based on DNA technology, and
CC with the use of the variants for the treatment of coagulation disorders
CC such as thrombosis or APC resistance, or in diagnostic test systems for
CC assaying components of the protein C-anticoagulant system (all claimed).
CC The variants may also be used in treating arteriosclerosis, myocardial
CC infarction, and disseminated intravascular coagulation. Note: The present
CC sequence is not shown in the specification but is derived from the human
CC wild-type Gla domain sequence given on page 7 of the specification (see
CC ABB79947)

XX SQ Sequence 45 AA;

Query Match 85.3%; Score 168; DB 5; Length 45;
Best Local Similarity 72.7%; Pred. No. 1.6e-20;
Matches 32; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 ANSFLXLRQGLXRCIXXICDFXXAXIFEDVDDTLAFWSKH 44
DB 1 ANSFLXLRQGLXRCIXXICDFXXAXIFEDVDDTLAFWSKH 44

Search completed: March 1, 2004, 10:01:23
Job time : 50 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2004, 09:59:33 ; Search time 13.5 Seconds
(without alignments)
313.513 Million cell updates/sec

Title: SEQ1-4SUBS
Perfect score: 197
Sequence: 1 ANSFLXLRggSLRXCIXX.....XXAKXIFedVDTLAFWSKH 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78.*

1: Piri:.*
2: Piri:.*
3: Piri:.*
4: Piri:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	160	81.2	461	1 KXHU	protein C (activat
2	140	71.1	461	1 JX0210	protein C (activat
3	139	70.6	461	1 S18894	protein C (activat
4	122	61.9	456	1 KXBO	coagulation factor
5	115	58.4	482	1 EXRT	coagulation factor
6	114	57.9	492	1 EXBO	coagulation factor
7	110	55.8	488	1 EXHU	coagulation factor
8	101	51.3	443	2 I46932	coagulation factor
9	99	50.3	466	1 KFHU7	coagulation factor
10	86.5	43.9	617	2 S10511	thrombin (EC 3.4.2
11	86.5	43.9	618	2 A35827	coagulation factor
12	86	43.7	475	1 EXCH	coagulation factor
13	85	43.1	407	1 KFB07	plasma protein S p
14	85	43.1	642	2 S53434	plasma protein S p
15	85	43.1	676	1 KXHU5	thrombin (EC 3.4.2
16	84	42.6	622	1 TBHU	plasma protein S -
17	81	41.1	646	2 S38819	coagulation factor
18	80	40.5	452	1 A30351	coagulation factor
19	80	40.6	459	2 JC0419	coagulation factor
20	80	40.6	461	1 KFHU	plasma protein S p
21	80	40.6	675	1 KXBOS	plasma protein S p
22	78	39.6	642	2 S53433	plasma protein S p
23	78	39.6	675	1 KXRTS	coagulation factor
24	73	37.1	416	1 KFB0	thrombin (EC 3.4.2
25	72	36.5	625	1 TBBO	plasma protein S p
26	71	36.0	675	1 KXMS	plasma protein 2 -
27	59.5	35.3	396	1 KXBOZ	plasma protein 2 -
28	55.5	33.2	422	1 KXHUZ	growth arrest-spec
29	65	33.0	673	2 A48089	

RESULT 1

KXHU

Protein C (activated) (EC 3.4.21.69) precursor - human
N:Alternate names: autoprothrombin IIA; plasma protein C

C:Species: Homo sapiens (man)
C>Date: 17-Mar-1987 #sequence revision 17-Mar-1987 #text_change 16-Jul-1999
C:Accession: A22331; A25426; A21781; A23789; A00927

R:FOster, D.C.; Yoshitake, S.; Davie, E.W.

Proc. Natl. Acad. Sci. U.S.A. 82, 4673-4677, 1985

A:Title: The nucleotide sequence of the gene for human protein C.

A:Reference number: A22331; MUID:85270390; PMID:2991887

A:Accession: A22331

A:Molecule type: DNA

A:Residues: 1-461 <FOS1>

A:Cross-references: GB:M11228; NID:g190333; PIDN:AAA60166.1; PID:g190334

R:Plutsky, J.; Hoskins, J.A.; Long, G.L.; Crabtree, G.R.

Proc. Natl. Acad. Sci. U.S.A. 83, 546-550, 1986

A:Title: Evolution and organization of the human protein C gene.

A:Reference number: A25426; MUID:86120978; PMID:3511471

A:Accession: A25426

A:Molecule type: DNA

A:Residues: 1-445, 'L', 446-461 <PLJ>

A:Cross-references: GB:M12712; NID:g190330; PIDN:AAA60165.1; PID:g190332

R:FOster, D.; Davie, E.W.

Proc. Natl. Acad. Sci. U.S.A. 81, 4766-4770, 1984

A:Title: Characterization of a cDNA coding for human protein C.

A:Reference number: A21781; MUID:84272714; PMID:6589623

A:Accession: A21781

A:Molecule type: mRNA

A:Residues: 'Q', 107-461 <FOS2>

A:Cross-references: GB:K02059; NID:g190322; PIDN:AAA60164.1; PID:g190323

R:Beckmann, R.J.; Schmidt, R.J.; Santerre, R.F.; Plutsky, J.; Crabtree, G.R.; Long, G.L.

Nucleic Acids Res. 13, 5233-5247, 1985

A:Title: The structure and evolution of a 461 amino acid human protein C precursor and i

A:Reference number: A23789; MUID:85269639; PMID:2991859

A:Accession: A23789

A:Molecule type: mRNA

A:Residues: 1-461 <BEC>

A:Cross-references: GB:X02750; NID:g35689; PIDN:CAA36528.1; PID:g763120

R:Miletich, J.P.; Broze Jr., G.J.

J. Biol. Chem. 265, 11397-11404, 1990

A:Title: Beta protein C is not glycosylated at asparagine 329. The rate of translation m

A:Reference number: A44605; MUID:90293094; PMID:1694179

A:Contents: annotation; carbohydrate binding sites; activation peptide

A:Note: The alpha form of protein C is glycosylated at Asn-329, and the beta form is not

R:Harris, R.J.; Ling, V.T.; Spellman, M.W.

J. Biol. Chem. 267, 5102-5107, 1992

A:Title: O-linked fucose is present in the first epidermal growth factor domain of facto:

A:Reference number: A44606; MUID:92184750; PMID:1544894

A:Contents: annotation; beta-hydroxyaspartic acid

C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that in

ivation of factor Va is strongly enhanced by complexing with protein S. Protein C also f:

growth potentiating
growth arrest-spec
probable MAP kinase
probable MAP kinase
probable MAP kinase
hypothetical prote
hypothetical prote
protein-tyrosine k
hypothetical prote
ammonium transport
mitogen-activated
VSG expression sit
protein-tyrosine k
platelet-derived g
tyrosine kinase re
type II site-speci

ALIGNMENTS

C:Comment: Protein C is synthesized in the liver as a single chain precursor, which is cleaved into two chains by a dodecapeptide from the amino end of the heavy chain; this reaction, which cleaves a dodecapeptide from the amino end of the heavy chain; this reaction.

C:Genetics:

A:Gene: GDB:PROC

A:Cross-references: GDB:120317; OMIM:176860

A:Map position: 2q13-2q21

A:Introns: 24/1; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1

C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C:Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding

F:1-32/Domain: signal sequence #status predicted <SIG>

F:27-86/Domain: Gla domain homology <Gla>

F:33-42/Domain: propeptide #status predicted <PRO>

F:43-197/Product: protein C light chain #status predicted <LCH>

F:92-131/Domain: EGF homology <EG1>

F:140-175/Domain: EGF homology <EG2>

F:200-461/Product: protein C heavy chain #status predicted <HCH>

F:200-211/Domain: activation peptide #status experimental <APT>

F:212-445/Domain: trypsin homology <TRY>

F:48-49,56,58,61,62,67,70/Modified site: gamma-carboxyglutamic acid (Glu) #status exp

F:59-64,92-105,101-120,122-131,140-151,147-160,162-175,183-319,238-254,373-387,398-426/Disulfide bonds: #status predicted

F:106-111/Disulfide bonds: #status predicted

F:113/Binding site: erythro-beta-hydroxyaspartic acid (Asp) #status absent

F:110/Binding site: carboxylate (Thr) (covalent) #status experimental

F:139,290,355/Binding site: carboxylate (Asn) (covalent) #status experimental

F:211-212/Cleavage site: Arg-Leu (thrombin) #status experimental

F:253,299,402/Active site: His, Asp, Ser #status predicted

F:371/Binding site: carboxylate (Asn) (covalent) (partial) #status atypical

Query Match 81.2%; Score 160; DB 1; Length 461;
Best Local Similarity 70.5%; Pred. No. 8.6e-18;
Matches 31; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 1 ANSFLXLRQSLXRXICIXICDFXXAKXIFEDVDDTLAFWSKH 44
Db 43 ANSFLXLRQSLXRXICIXICDFXXAKXIFEDVDDTLAFWSKH 86

RESULT 2

protein C (activated) (EC 3.4.21.69) precursor - mouse
N:Alternate names: vitamin K-dependent serine proteinase
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: JX0210
R:Tada, N.; Sato, M.; Tsujimura, A.; Iwase, R.; Hashimoto-Gotoh, T.
J. Biochem. 111, 491-495, 1992
A:Title: Isolation and characterization of a mouse protein C cDNA.
A:Reference number: JX0210; MUID:92316897; PMID:1618739
A:Accession: JX0210

A:Molecule type: mRNA
A:Residues: 1-461 <TAD>
A:Cross-references: GB:D10445; NID:G220385; PIDN:BA01235.1; PID:G220386
A:Experimental source: liver
C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that re
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglut
F:1-33/Domain: signal sequence #status predicted <SIG>
F:27-85/Domain: Gla domain homology <Gla>
F:34-41/Domain: propeptide #status predicted <PRO>
F:42-186,199-461/Product: protein C #status predicted <PRC>
F:43-186/Domain: light chain #status predicted <PCL>
F:91-130/Domain: EGF homology <EG1>
F:139-174/Domain: EGF homology <EG2>
F:199-461/Domain: heavy chain #status predicted <PCH>
F:199-211/Domain: activation peptide #status predicted <ACT>
F:212-461/Product: vitamin K-dependent serine proteinase #status predicted <VIN>
F:212-445/Domain: trypsin homology <TRY>
F:47,48,55,57,60,61,66,67,70/Modified site: gamma-carboxyglutamic acid (Glu) #status
F:121,130,139-150,146-159,161-174,182-320,239-255,373-387,398-426/Disulfide bonds: #stat
F:214,290,355/Binding site: carboxylate (Asn) (covalent) #status predicted
F:253,299,402/Active site: His, Asp, Ser #status predicted

Query Match 71.1%; Score 140; DB 1; Length 461;
Best Local Similarity 59.1%; Pred. No. 1.5e-14;
Matches 26; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 1 ANSFLXLRQSLXRXICIXICDFXXAKXIFEDVDDTLAFWSKH 44
Db 42 ANSFLXLRQSLXRXICIXICDFXXAKXIFEDVDDTLAFWSKH 85

RESULT 3

protein C (activated) (EC 3.4.21.69) precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 29-Oct-1999
C:Accession: S18994; S24312
R:Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.
submitted to the EMBL Data Library, February 1992
A:Description: The cDNA cloning and mRNA expression of rat protein C.
A:Reference number: S18994
A:Accession: S18994
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-461 <OKA>
A:Cross-references: EMBL:X64336; NID:G56962; PIDN:CAA45617.1; PID:G56963
R:Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.
Biochim. Biophys. Acta 1131, 329-332, 1992
A:Title: The cDNA cloning and mRNA expression of rat protein C.
A:Reference number: S24312; MUID:92329550; PMID:1627650
A:Accession: S24312
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-461 <OKA2>
A:Cross-references: EMBL:X64336; NID:G56962; PIDN:CAA45617.1; PID:G56963
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid; glycoprotein; hydrolyase; serine proteinase
F:1-32/Domain: signal sequence #status predicted <SIG>
F:27-85/Domain: Gla domain homology <Gla>
F:33-42/Domain: propeptide #status predicted <PRO>
F:43-461/Product: protein C #status predicted <PRC>
F:91-130/Domain: EGF homology <EG1>
F:139-174/Domain: EGF homology <EG2>
F:139-445/Domain: trypsin homology <TRY>
F:47,48,55,57,60,61,66,67,70/Modified site: gamma-carboxyglutamic acid (Glu) #status
F:121,130,139-150,146-159,161-174,182-320,239-255,373-387,398-426/Disulfide bonds: #stat
F:215,291,355/Binding site: carboxylate (Asn) (covalent) #status predicted
F:254,300,402/Active site: His, Asp, Ser #status predicted

Query Match 70.6%; Score 139; DB 1; Length 461;
Best Local Similarity 59.1%; Pred. No. 2.1e-14;
Matches 26; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 1 ANSFLXLRQSLXRXICIXICDFXXAKXIFEDVDDTLAFWSKH 44
Db 42 ANSFLXLRQSLXRXICIXICDFXXAKXIFEDVDDTLAFWSKH 85

RESULT 4

protein C (activated) (EC 3.4.21.69) precursor - bovine (fragment)
N:Alternate names: autoprothrombin IIA; plasma protein C
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Nov-1980 #sequence_revision 17-Mar-1987 #text_change 16-Jul-1999
C:Accession: A26250; A19385; A18386; A00928
R:Long, G.L.; Balgaj, R.M.; Macgillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 81, 5653-5656, 1984
A:Title: Cloning and sequence of liver cDNA coding for bovine protein C.
A:Reference number: A26250; MUID:85014836; PMID:6091100
A:Accession: A26250
A:Molecule type: mRNA
A:Residues: 1-456 <LON>
R:Penlund, P.; Stenflo, J.

A;Accession: S49075
A:Molecule type: mRNA
A;Residues: 1-482 <STAL>
A;Cross-references: EMBL:X79807; NID:g506600; PIDN:CAA56202.1; PID:g506601
A;Note: submitted to the EMBL Data Library, June 1994
R;Stanton, C.; Ross, R.P.; Hutson, S.; Wallin, R.
Gene 159, 269-273, 1996
A;Title: Processing and expression of rat and human clotting factor X-encoding cDNAs.
A;Reference number: JC4670; MUID:96194815; PMID:8647460
A;Accession: JC4670
A:Molecule type: mRNA
A;Residues: 1-482 <STA2>
A;Cross-references: EMBL:X79807; NID:g506600; PIDN:CAA56202.1; PID:g506601
A;Experimental source: Cos-1 cell
R;Enjyoji, K.; Miyazaki, K.; Kato, H.
J. Biochem. 109, 890-898, 1991
A;Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat plasma
A;Reference number: PS0190; MUID:92041742; PMID:1718949
A;Accession: PS0191
A:Molecule type: protein
A;Residues: 41-58,'X',50-65 <ENL1>
A;Accession: PS0190
A:Molecule type: protein
A;Residues: 183-186,'X',188-207 <ENJ2>
R;Murakawa, M.; Okamura, T.; Kamura, T.; Kuratsune, M.; Harada, M.; Niho, Y.
Eur. J. Haematol. 52, 162-168, 1994
A;Title: Analysis of the partial nucleotide sequences and deduced primary structures of:
A;Reference number: I46136; MUID:94222160; PMID:8168596
A;Accession: I62745
A>Status: preliminary; translated from GB/EMBL/DDBB
A:Molecule type: DNA
A;Residues: 295-383,'G',385-455 <MUR>
A;Cross-references: GB:D21215; NID:g415309; PIDN:BAA04756.1; PID:g455396
C;Function:
A;Description: catalyzes the proteolytic activation of prothrombin to thrombin in the presence of Factor V
A;Pathway: blood coagulation
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamate
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-40/Domain: propeptide #status predicted <PRO>
F;25-84/Domain: Gla domain homology <GLA>
F;41-179/Product: coagulation factor X light chain #status predicted <LCH>
F;90-121/Domain: EGF homology <EG1>
F;129-164/Domain: EGF homology <EG2>
F;183-482/Product: coagulation factor X heavy chain #status predicted <HCH>
F;183-231/Domain: activation peptide #status predicted <APT>
F;232-482/Product: coagulation factor Xa heavy chain #status predicted <ACT>
F;233-460/Domain: trypsin homology <TRY>
F;46,47,54,56,59,60,65,66,69,77,79/Modified site: gamma-carboxyglutamic acid (Glu) #status predicted <GCM>
F;57-62,90-101,95-110,112-121,129-140,136-149,151-164,172-340,238-243,259-275,388-402,411-412/Binding site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted <ASP>
F;103/Modified site: carbohydurate (Asn) (covalent) #status experimental
F;187/Binding site: carbohydurate (Asn) (covalent) #status experimental
F;208/Binding site: carbohydurate (Asn) (covalent) #status predicted
F;218/Binding site: carbohydurate (Asn) (covalent) #status predicted
F;231-232/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #status predicted
F;274,320,417/Active site: His, Asp, Ser #status predicted

Query Match 58.4%; Score 115; DB 1; Length 482;
Best Local Similarity 43.2%; Pred. No. 1.6e-10;
Matches 19; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

DDBD 1 ANSPXXLRGSLRXRCIXXCIFDCFXAKXIFEVDVDTLAFWSKH 44
|||||:::|||||:::|||||:::|||||:::|||||::||
41 ANSFFEEKGNLERECVEICSFSEAREVFEDNEKTEFWNKY 84

RESULT 6
COAGULATION
Coagulation factor Xa (EC 3.4.21.6) precursor - bovine
Alternate names: Stuart factor
Species: Bos primigenius taurus (cattle)
Date: 24-Apr-1984 #sequence revision 17-Mar-1987 #text change 16-Jul-1999

C;Accession: A22867; A14997; A12030; A34412; S39414; A00925
R;Fung, M.R.; Campbell, R.M.; MacGillivray, T.A.
Nucleic Acids Res. 12, 4481-4492, 1984
A;Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containing a
A;Reference number: A22867; MUID:84247315; PMID:6330671
A;Accession: A22867
A;Molecule type: mRNA
A;Residues: 1-487 <FUN>
A;Cross-references: GB:X00673; NID:G193; PIDN:CAA25286.1; PID:G193
R;Enfield, D.L.; Ericsson, L.H.; Fujikawa, K.; Walsh, K.A.; Neurath, H.; Titani, K.
Biochemistry 19, 659-667, 1980
A;Title: Amino acid sequence of the light chain of bovine factor X-1 (Stuart factor).
A;Reference number: A14997; MUID:80130563; PMID:6766735
A;Accession: A14997
A;Molecule type: protein
A;Residues: 41-102, 'N', 104-180 <ENF>
R;McMullen, B.A.; Fujikawa, K.; Kisiel, W.
Biochem. Biophys. Res. Commun. 115, 8-14, 1983
A;Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coagulation factors.
A;Reference number: A20274; MUID:8330813; PMID:6688526
A;Contents: annotation; revision to residue 103
R;Titani, K.; Fujikawa, K.; Enfield, D.L.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.
Proc. Natl. Acad. Sci. U.S.A. 72, 3082-3086, 1975
A;Title: Bovine factor X-1 (Stuart factor): amino-acid sequence of heavy chain.
A;Reference number: A12030; MUID:76053063; PMID:1059033
A;Accession: A12030
A;Molecule type: protein
A;Residues: 183-292, 294-295, 'GDE', 299-334, 336-348, 'AE', 351-354, 356-441, 'GKFG', 446-492 <T>
A;Note: carboxylate binding sites and disulfide bonds were determined
R;Persson, E.; Selander, M.; Linse, S.; Drakenberg, T.; Oehlin, A.K.; Stenflo, J.
J. Biol. Chem. 264, 16897-16904, 1989
A;Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epidermal
A;Reference number: A34412; MUID:89380326; PMID:2789221
A;Accession: A34412
A;Molecule type: protein
A;Residues: 85-126 <PER>
A;Note: beta-hydroxyaspartic acid site
R;Inoue, K.; Morita, T.
Eur. J. Biochem. 218, 153-163, 1993
A;Title: Identification of O-linked oligosaccharide chains in the activation peptides of
A;Reference number: S39414; MUID:94062825; PMID:8243461
A;Accession: S39414
A;Molecule type: protein
A;Residues: 183-196;199-209;216-233 <INO>
A;Note: carboxylate binding sites
R;Titani, K.; Hermanson, M.A.; Fujikawa, K.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.; D
Biochemistry 11, 4899-4903, 1972
A;Title: Bovine factor X-1a (activated Stuart factor). Evidence of homology with mammal
A;Reference number: A12453; MUID:73053314; PMID:4264286
A;Contents: annotation; active site
R;Fujikawa, K.; Titani, K.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 72, 3359-3363, 1975
A;Title: Activation of bovine factor X (Stuart factor): conversion of factor Xaalpha to
A;Reference number: A13504; MUID:76053121; PMID:1059122
A;Contents: annotation; activation
R;Sugo, T.; Bjork, I.; Holmgren, A.; Stenflo, J.
J. Biol. Chem. 259, 5705-5710, 1984
A;Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxyglutamic
A;Reference number: A38024; MUID:84185716; PMID:6546930
A;Contents: annotation; calcium binding
R;Morita, T.; Jackson, C.M.
J. Biol. Chem. 261, 4008-4014, 1986
A;Reference number: A38025; MUID:96140210; PMID:3949800
A;Contents: annotation; sulfate binding
C;Comment: Factor Xa converts prothrombin to thrombin during blood clotting.
C;Comment: The two chains are formed from a single-chain precursor by the excision of two
C;Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway), C
activation.
C;Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with str
C;Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin
C;Genetic:
A;Gene: F10
A;Map position: 13q34

C;Function:
A;Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr
A;Pathway: blood coagulation
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam
F1-15/Domain: signal sequence #status predicted <SIG>
F16-40/Domain: propeptide #status predicted <PRO>
F25-84/Domain: Gla domain homology <GUA>
F41-180/Product: coagulation factor X light chain #status experimental <LCH>
F90-121/Domain: EGF homology <EG1>
F129-164/Domain: EGF homology <EG2>
F183-492/Product: coagulation factor X heavy chain #status experimental <HCH>
F183-233/Domain: activation peptide #status experimental <APT>
F234-492/Product: coagulation factor Xa heavy chain #status experimental <AHC>
F234-461/Domain: trypsin homology <TRY>
F46,47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu) #s
F57-62,90,101,95-110,112-121,129-140,136-149,151-164,172-341/Disulfide bonds: #status p
F103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F200/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental
F208,485/Binding site: carbohydrate (Thr) (covalent) #status experimental
F218/Binding site: carbohydrate (Asn) (covalent) #status experimental
F233-234/Cleavage site: Arg-116 (coagulation factor IXa, coagulation factor VIIa) #stat
F240-245,250-278,389-403,414-442/Disulfide bonds: #status experimental
F275,321,418/Active site: His, Asp, Ser #status predicted
Query Match 57.9%; Score 114; DB 1; Length 492;
Best Local Similarity 45.5%; Pred. No. 2.4e-10;
Matches 20; Conservative 8; Mismatches 16; Indels 0; Gaps 0;
QY 1 ANSTLXLRLQSLRXKICIXICDFXXAKXIFEDVDDTLAPWSKH 44
Db 41 ANSFLEVKQGNRECLLEACSLSEAREVFEDAEQTFDFWSKY 84
RESULT 7
EXHU
coagulation factor Xa (EC 3.4.21.6) precursor [validated] - human
N;Alternate names: Stuart factor
C;Species: Homo sapiens (man)
C;Date: 15-Nov-1984 #sequence revision 02-May-1994 #text change 08-Dec-2000
A;Accession: A24478; JQ0917; A42485; A25853; A22208; A21284; A20362; S39415; I54051; A00
R;Leytus, S.P.; Foster, D.C.; Kurachi, K.; Davie, E.W.
Biochemistry 25, 5098-5102, 1986
A;Title: Gene for human Factor X: a blood coagulation factor whose gene organization is
A;Reference number: A24478; MUID:87026500; PMID:3768336
A;Accession: A24478
A;Molecule type: DNA
A;Residues: 1-488 <LBY>
A;Cross-references: GB:L29433; GB:M14327; NID:9459809; PIDN:AAA52764.1; PID:G182831
R;Messier, T.L.; Pittman, D.D.; Long, G.L.; Kaufman, R.J.; Church, W.R.
Gene 99, 291-294, 1991
A;Title: Cloning and expression in COS-1 cells of a full-length cDNA encoding human coag
A;Reference number: JQ0917; MUID:91216473; PMID:1902434
A;Accession: JQ0917
A;Molecule type: mRNA
A;Residues: 1-488 <MES>
R;Miao, C.H.; Leytus, S.P.; Chung, D.W.; Davie, E.W.
J. Biol. Chem. 267, 7395-7401, 1992
A;Title: Liver-specific expression of the gene coding for human factor X, a blood coagul
A;Reference number: A42485; MUID:92218390; PMID:1313796
A;Accession: A42485
A;Molecule type: DNA
A;Residues: 1-15 <MIA>
A;Experimental source: liver
A;Note: sequence extracted from NCBI backbone (NCBI:93780, NCBI:93787)
R;Kaul, R.K.; Hildebrand, B.; Roberts, S.; Jagadeeswaran, P.
Gene 41, 311-314, 1986
A;Title: Isolation and characterization of human blood-coagulation factor X cDNA.
A;Reference number: A25853; MUID:86221713; PMID:3011603
A;Accession: A25853
A;Molecule type: mRNA
A;Residues: 19-284, 'E', 289-488 <KAU>

F;103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F;199,211/Binding site: carbohydrate (Thr) (covalent) #status experimental
F;221,231/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;234-235/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #stat
F;276,322,419/Active site: His, Asp, Ser #status experimental

Query Match 55.8%; Score 110; DB 1; Length 488;
Best Local Similarity 43.2%; Pred. No. 1.1e-09;
Matches 19; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANSFLXLRGSLRXRCIXXCIDEXKAKXFEDVDITLAFWSKH 44
||||| :||| :||| :||| :||| :||| :||| :||| :
Db 41 ANSLEENKKHLEBCEMEICSYEARREVFDSDKTNEFWNKY 84

RESULT 8
I46932
coagulation factor VII - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 12-Feb-1999
C:Accession: I46932
R:Brothers, A.B.; Clarke, B.J.; Sheffield, W.P.; Blajchman, M.A.
Thromb. Res. 69, 231-238, 1993
A>Title: Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII
A:Reference number: I46932; MUID:93190306; PMID:8383365
A:Accession: I46932
A>Status: preliminary; translated from GB/EMBL/DBSJ
A:Molecule type: mRNA
A:Residues: 1-443

A:Cross-references: GB:S56300; NID:g256294; PID:g266295
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
F;24-83/Domain: Gla domain homology <LA>
F;89-120/Domain: EGF homology <EG1>
F;130-166/Domain: EGF homology <EG2>
F;192-425/Domain: trypsin homology <TRY>

Query Match 51.3%; Score 101; DB 2; Length 443;
Best Local Similarity 46.3%; Pred. No. 2.7e-08;
Matches 19; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

QY 1 ANSFLXLRGSLRXRCIXXCIFXXAXKFEDVDDTLAFW 41
||||| |||| |::| ::||| :||| :||| :||| :||| :||| :
Db 40 ANSFLELPGLRECKELCSFEAREVFQSTERTKQFW 80

RESULT 9
KPNU7
coagulation factor VIIa (EC 3.4.21.21) precursor [validated] - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1989 #sequence_revision 19-May-1994 #text_change 08-Dec-2000
C:Accession: A28322; A2819; A31186; B31186; S63524
R;O'Hara, P.J.; Grant, F.J.; Haldegarn, B.A.; Gray, C.L.; Insley, M.Y.; Hagen, F.S.; Murr
Proc. Natl. Acad. Sci. U.S.A. 84, 5158-5162, 1987
A>Title: Nucleotide sequence of the gene coding for human factor VII, a vitamin K-depend
A:Reference number: A28322; MUID:87260948; PMID:3037537
A:Accession: A28322
A:Molecule type: DNA
A:Residues: 1-466 <OH>
A:Cross-references: GB:J02933; NID:g180333; PIDN:AAA51983.1; PID:g1820334
R:Hagen, F.S.; Gray, C.L.; O'Hara, P.J.; Grant, F.J.; Saari, G.C.; Woodbury, R.G.; Hart, C
Proc. Natl. Acad. Sci. U.S.A. 83, 2412-2416, 1986
A>Title: Characterization of a cDNA coding for human factor VII.
A:Reference number: A23819; MUID:86205965; PMID:3486420
A:Accession: A23819
A:Molecule type: mRNA
A:Residues: 1-466 <HA>
A:Cross-references: GB:M13232; NID:g182799; PIDN:AAA88040.1; PID:g182801
R,Thim, L.; Bjornsen, S.; Christensen, M.; Nicolaisen, E.M.; Lund-Hansen, T.; Pedersen, A.I
Biochemistry 27, 7785-7793, 1988
A>Title: Amino acid sequence and posttranslational modifications of human factor VII-a f
A:Reference number: A90539; MUID:89088153; PMID:3264725
A:Accession: A31186
A:Molecule type: protein

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2004, 09:58:27 ; Search time 10.5 Seconds
(without alignments)
218.199 Million cell updates/sec

Title: SEQ1-4SUBS

Perfect score: 197

Sequence: 1 ANSFLXLRGGSLRXRCIXX.....XXAKXIFedVDTIAFWSKH 44

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	160	81.2	461	1 PRTC_HUMAN	P04070 homo sapien
2	140	71.1	461	1 PRTC_MOUSE	P33587 mus musculus
3	139	70.6	461	1 PRTC_RAT	P31394 rattus norv
4	138	70.1	458	1 PRTC_RABIT	Q28661 oryctolagus
5	123	62.4	459	1 PRTC_PIG	Q961p2 sus scrofa
6	122	61.9	456	1 PRTC_BOVIN	P00745 bos taurus
7	114	57.9	492	1 FA10_BOVIN	P00743 bos taurus
8	110	55.8	488	1 FA10_HUMAN	P00742 homo sapien
9	107	54.3	231	1 TMG3_HUMAN	Q9Bzd7 homo sapien
10	103	52.3	490	1 FA10_RABIT	Q19045 oryctolagus
11	101	51.3	444	1 FA7_RABIT	P98139 oryctolagus
12	99	50.3	466	1 FA7_HUMAN	P08709 homo sapien
13	92	46.7	218	1 TMG1_HUMAN	O14668 homo sapien
14	86.5	43.9	617	1 THRE_RAT	P18292 rattus norv
15	86.5	43.9	618	1 THRE_MOUSE	P19221 mus musculus
16	86	43.7	475	1 FA10_CHICK	P25155 gallus gall
17	85	43.1	407	1 FA7_BOVIN	P22457 bos taurus
18	85	43.1	649	1 PRTS_MACMU	Q28520 macaca mula
19	85	43.1	676	1 PRTS_HUMAN	Q9Bzd6 homo sapien
20	84.5	42.9	226	1 TMG4_HUMAN	P07225 homo sapien
21	84	42.6	376	1 FA10_HOPST	P83370 hoplocephal
22	84	42.6	622	1 THRE_HUMAN	P00734 homo sapien
23	82	41.6	376	1 FA10_TROCA	P81428 tropidichis
24	81	41.1	646	1 PRTS_RABIT	P98118 oryctolagus
25	80	40.6	446	1 FA7_MOUSE	P70375 mus musculus
26	80	40.6	452	1 FA9_CANFA	P19540 canis famil
27	80	40.6	459	1 FA9_MOUSE	P16294 mus musculus
28	80	40.6	461	1 FA9_HUMAN	P00740 homo sapien
29	80	40.6	461	1 FA9_PANTR	Q95nd7 pan troglod
30	80	40.6	675	1 PRTS_BOVIN	P07224 bos taurus
31	78	39.6	675	1 PRTS_RAT	P53813 rattus norv
32	73	37.1	416	1 FA9_BOVIN	P00741 bos taurus
33	72	36.5	98	1 FA10_NOTCH	P82807 notechis sc

RESULT 1

ID	PRTC_HUMAN	STANDARD;	PRT;	461 AA.
AC	P04070; Q15189; Q15190; Q16001;			
DT	01-NOV-1986 (Rel. 03, Created)			
DT	01-NOV-1986 (Rel. 03, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Vitamin-K-dependent protein C precursor (EC 3.4.21.69)			
DE	(Antopthrombin IIA) (Anticoagulant protein C) (Blood coagulation factor XIV).			
DE	PROCC.			
GN	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
[1]	SEQUENCE FROM N.A.			
RP	MEDLINE=85270390; PubMed=2991887;			
RX	Poster D.C., Yoshitake S., Davie E.W.;			
RA	"The nucleotide sequence of the gene for human protein C.;"			
RL	Proc. Natl. Acad. Sci. U.S.A. 82:4673-4677(1985).			
[2]	SEQUENCE FROM N.A.			
RP	MEDLINE=85269639; PubMed=2991859;			
RX	Beckmann R.J., Schmidt R.J., Santerre R.F., Plutzky J., Crabtree G.R.,			
RA	Long G.L.;			
RT	"The structure and evolution of a 461 amino acid human protein C			
RT	precursor and its messenger RNA, based upon the DNA sequence of			
RT	cloned human liver cDNAs.;"			
RL	Nucleic Acids Res. 13:5233-5247(1985).			
[3]	SEQUENCE FROM N.A.			
RP	MEDLINE=86120978; PubMed=3511471;			
RX	Plutzky J., Hoskins J.A., Long G.L., Crabtree G.R.;			
RA	"Evolution and organization of the human protein C gene.;"			
RL	Proc. Natl. Acad. Sci. U.S.A. 83:546-550(1986).			
[4]	SEQUENCE FROM N.A.			
RP	Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,			
RA	Nickerson D.A.;			
RL	Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.			
[5]	SEQUENCE FROM N.A.			
RP	TISSUE=Colon;			
RC	MEDLINE=22388557; PubMed=12477932;			
RX	Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klitscher R.D., Collins F.S., Wagner L., Shenmen C.N., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Scapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Lomeli N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			

ALIGNMENTS

P00735 bos taurus
Q08761 mus musculus
P00744 bos taurus
P22891 homo sapien
O14669 homo sapien
P43068 candida alb
Q95W2 toxoplasma
Q9H270 homo sapien
Q91W86 mus musculus
P35917 mus musculus
Q9Y493 homo sapien
Q92398 schizosach

34 72 36.5 625 1 THRB_BOVIN
35 71 36.0 675 1 PRTS_MOUSE
36 69.5 35.3 396 1 PRTZ_BOVIN
37 65.5 33.2 400 1 PRTZ_HUMAN
38 65 33.0 202 1 TMG2_HUMAN
39 52 26.4 501 1 MKC1_CANAL
40 50 25.4 363 1 ADK_TOKGO
41 49.5 25.1 941 1 VPIL_HUMAN
42 49.5 25.1 941 1 VPIL_MOUSE
43 49 24.9 1363 1 VGR3_MOUSE
44 49 24.9 2812 1 ZAN_HUMAN
45 48 24.4 422 1 SPMI_SCHPO

RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP SEQUENCE OF 106-461 FROM N.A.
RX MEDLINE=84272714; PubMed=6589623;
RA Foster D.C., Davie E.W.;
RT "Characterization of a cDNA coding for human protein C.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984).
RN [7]
RP CARBOHYDRATE-LINKAGE SITE ASN-371.
RX MEDLINE=90293094; PubMed=1694179;
RA Milletich J.P., Broze G.J. Jr.;
RT "Beta protein C is not glycosylated at asparagine 329. The rate of
RT translation may influence the frequency of usage at asparagine-X-
RT cysteine sites.";
RL J. Biol. Chem. 265:11397-11404(1990).
RN [8]
RP HYDROXYLATION.
RX MEDLINE=92184750; PubMed=1544894;
RA Harris R.J., Ling V.T., Spellman M.W.;
RT "O-linked fucose is present in the first epidermal growth factor
RT domain of factor XII but not protein C.";
RL J. Biol. Chem. 267:5102-5107(1992).
RN [9]
RP 3D-STRUCTURE MODELING OF 175-450.
RX MEDLINE=94272342; PubMed=8003977;
RA Fisher C.L., Greengard J.S., Griffin J.H.;
RT "Models of the serine protease domain of the human antithrombotic
RT plasma factor activated protein C and its zymogen.";
RL Protein Sci. 3:588-599(1994).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 84-461.
RX MEDLINE=97157472; PubMed=9003757;
RA Mather T., Oganessyan V., Hof P., Huber R., Foundling S., Esmen C.,
RA Bode W.;
RT "The 2.8 A crystal structure of Gla-domainless activated protein C.";
RL EMBO J. 15:6822-6831(1996).
RN [11]
RP REVIEW ON PROC VARIANTS.
RX MEDLINE=93190290; PubMed=8446940;
RA Reitsma P.H., Poort S.R., Bernardi F., Gandrille S., Long G.L.,
RA Sala N., Cooper D.N.;
RT "Protein C deficiency: a database of mutations. For the Protein C & S
RT Subcommittee of the Scientific and Standardization Committee of the
RT International Society on Thrombosis and Haemostasis.";
RL Thromb. Haemost. 69:77-84(1993).
RN [12]
RP VARIANT PROC DEFICIENCY CYS-444.
RX MEDLINE=87204221; PubMed=2437584;
RA Romeo G., Hassan H.J., Scaemphil S., Roncuzzi L., Cianetti L.,
RA Leonardi A., Vicente V., Mannucci P.M., Bertina R.M., Peschle C.,
RA Cortese R.;
RT "Hereditary thrombophilia: identification of nonsense and missense
RT mutations in the protein C gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:2829-2832(1987).
RN [13]
RP VARIANT PROC DEFICIENCY TRP-211.
RX MEDLINE=90098906; PubMed=2602169;
RA Grundy C.B., Chitole A., Talbot S., Bevan D., Kakkar V.V.,
RA Cooper D.N.;
RT "Protein C London 1: recurrent mutation at Arg-169 (CGG-->TGG) in
RT the protein C gene causing thrombosis.";
RL Nucleic Acids Res. 17:10513-10513(1989).
RN [14]
RP VARIANT PROC DEFICIENCY CYS-272.
RX MEDLINE=91329836; PubMed=1868249;

RA Reitsma P.H., Poort S.R., Allaart C.F., Briet E., Bertina R.M.;
RT "The spectrum of genetic defects in a panel of 40 Dutch families with
RT symptomatic protein C deficiency type I: heterogeneity and founder
RT effects.";
RL Blood 78:890-894(1991).
RN [15]
RP VARIANTS PROC DEFICIENCY ALA-62 AND MET-76.
RX MEDLINE=92190481; PubMed=1347706;
RA Bovill E.G., Tomczak J.A., Grant B., Bhushan F., Pillemer E.,
RA Rainville I.R., Long G.L.;
RT "Protein Cwermt: symptomatic type II protein C deficiency
RT associated with two GLA domain mutations.";
RL Blood 79:1456-1465(1992).
RN [16]
RP VARIANT PROC DEFICIENCY ASP-418.
RX MEDLINE=92305321; PubMed=1611081;
RA Sugihara Y., Miura O., Yuen P., Aoki N.;
RT "Protein C deficiency Hong Kong 1 and 2: hereditary protein C
RT deficiency caused by two mutant alleles, a 5-nucleotide deletion and
RT a missense mutation.";
RL Blood 80:126-133(1992).
RN [17]
RP VARIANT PROC DEFICIENCY LEU-289.
RX MEDLINE=92380660; PubMed=1511986;
RA Grundy C.B., Chisholm M., Kakkar V.V., Cooper D.N.;
RT "A novel homozygous missense mutation in the protein C (PROC) gene
RT causing recurrent venous thrombosis.";
RL Hum. Genet. 89:683-684(1992).
RN [18]
RP VARIANTS PROC DEFICIENCY GLN-220 AND TRP-220.
RX MEDLINE=92380661; PubMed=1511989;
RA Grundy C.B., Schulman S., Tengborn L., Kakkar V.V., Cooper D.N.;
RT "Two different missense mutations at Arg 178 of the protein C (PROC)
RT gene causing recurrent venous thrombosis.";
RL Hum. Genet. 89:685-686(1992).
RN [19]
RP VARIANT PROC DEFICIENCY GLN-220.
RX MEDLINE=92350852; PubMed=1301959;
RA Gandrille S., Vidaud M., Alach M., Alhenc-Gelas M., Fischer A.M.,
RA Gouault-Heilman M., Toulon P., Flessinger J.N., Goossens M.;
RT "Two novel mutations responsible for hereditary type I protein C
RT deficiency: characterization by denaturing gradient gel
RT electrophoresis.";
RL Hum. Mutat. 1:491-500(1992).
RN [20]
RP VARIANT PROC DEFICIENCY SER-334.
RX MEDLINE=92276939; PubMed=1593215;
RA Yamamoto K., Matsushita T., Sugiura I., Takamatsu J., Iwasaki E.,
RA Wada H., Deguchi K., Shirakawa S., Saito H.;
RT "Homozygous protein C deficiency: identification of a novel missense
RT mutation that causes impaired secretion of the mutant protein C.";
RL J. Lab. Clin. Med. 119:682-689(1992).
RN [21]
RP VARIANTS PROC DEFICIENCY TRP-38; CYS-42; HIS-42; GLN-271 AND ASN-294.
RX MEDLINE=93313192; PubMed=8324221;
RA Gandrille S., Alhenc-Gelas M., Gausem P., Aillaud M.-F., Dupuy E.,
RA Juhan-Vague I., Aiach M.;
RT "Five novel mutations located in exons III and IX of the protein C
RT gene in patients presenting with defective protein C anticoagulant
RT activity.";
RL Blood 82:159-168(1993).
RN [22]
RP VARIANTS PROC DEFICIENCY GLY-14; GLN-211; TYR-244; GLN-253; LEU-321;
RX CYS-328; ILE-385; THR-388 AND VAL-388.
RX MEDLINE=93271391; PubMed=8499565;
RA Poort S.R., Pabinger-Fasching I., Mannhalter C., Reitsma P.H.,
RA Bertina R.M.;
RT "Twelve novel and two recurrent mutations in 14 Austrian families
RT with hereditary protein C deficiency.";
RL Blood Coagul. Fibrinolysis 4:273-280(1993).
RN [23]
RP VARIANT PROC DEFICIENCY TRP-57.
RX MEDLINE=93271396; PubMed=8499568;

modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announcement> or send an email to license@isb-sib.ch).

EMBL; X64336; CAA45617.1; -
FIR; S18994; S18994.
MEROPS; S01.218; -
InterPro; IPR000152; Asx hydroxyl S.
InterPro; IPR009003; Cys_ser_trypsin.
InterPro; IPR001881; EGF_Ca_-trypsin.
InterPro; IPR006209; EGF_like.
InterPro; IPR002383; GLA_blood.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase S1A.
InterPro; IPR000294; VitK_dep_GLA.
Pfam; PF00008; EGF; 2.
Pfam; PF00594; gla; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PRO0722; CHYMOTRYPSIN.
PRINTS; PRO0001; GLABLOOD.
SMART; SM00179; EGF_CA; 1.
SMART; SM00069; GLA; 1.
SMART; SM00020; Tryp_Spc; 1.
PROSITE; PS00010; ASX_HYDROXYL; 1.
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS00026; EGF_3; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS00011; GLU_CARBOXYLATION; 1.
PROSITE; PS02040; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Blood coagulation; Glycoprotein; Serine protease;
Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
SIGNAL 1 32
PROPEP 33 41
CHAIN 42 196
CHAIN 199 461
PEPTIDE 199 212
SITE 212 213
DOMAIN 96 131
DOMAIN 135 175
DOMAIN 213 461
MOD_RES 47 47
MOD_RES 48 48
MOD_RES 55 55
MOD_RES 57 57
MOD_RES 60 60
MOD_RES 61 61
MOD_RES 66 66
MOD_RES 67 67
MOD_RES 70 70
MOD_RES 112 112
MOD_RES 254 254
ACT_SITE 300 300
ACT_SITE 402 402
DISULFID 58 63
DISULFID 91 110
DISULFID 100 105
DISULFID 104 119
DISULFID 121 130
DISULFID 139 150

CC modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announcement> or send an email to license@isb-sib.ch).

EMBL; X64336; CAA45617.1; -
FIR; S18994; S18994.
MEROPS; S01.218; -
InterPro; IPR000152; Asx hydroxyl S.
InterPro; IPR009003; Cys_ser_trypsin.
InterPro; IPR001881; EGF_Ca_-trypsin.
InterPro; IPR006209; EGF_like.
InterPro; IPR002383; GLA_blood.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase S1A.
InterPro; IPR000294; VitK_dep_GLA.
Pfam; PF00008; EGF; 2.
Pfam; PF00594; gla; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PRO0722; CHYMOTRYPSIN.
PRINTS; PRO0001; GLABLOOD.
SMART; SM00179; EGF_CA; 1.
SMART; SM00069; GLA; 1.
SMART; SM00020; Tryp_Spc; 1.
PROSITE; PS00010; ASX_HYDROXYL; 1.
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS00026; EGF_3; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS00011; GLU_CARBOXYLATION; 1.
PROSITE; PS02040; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Blood coagulation; Glycoprotein; Serine protease;
Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
SIGNAL 1 32
PROPEP 33 41
CHAIN 42 196
CHAIN 199 461
PEPTIDE 199 212
SITE 212 213
DOMAIN 96 131
DOMAIN 135 175
DOMAIN 213 461
MOD_RES 47 47
MOD_RES 48 48
MOD_RES 55 55
MOD_RES 57 57
MOD_RES 60 60
MOD_RES 61 61
MOD_RES 66 66
MOD_RES 67 67
MOD_RES 70 70
MOD_RES 112 112
MOD_RES 254 254
ACT_SITE 300 300
ACT_SITE 402 402
DISULFID 58 63
DISULFID 91 110
DISULFID 100 105
DISULFID 104 119
DISULFID 121 130
DISULFID 139 150

CC modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announcement> or send an email to license@isb-sib.ch).

EMBL; X64336; CAA45617.1; -
FIR; S18994; S18994.
MEROPS; S01.218; -
InterPro; IPR000152; Asx hydroxyl S.
InterPro; IPR009003; Cys_ser_trypsin.
InterPro; IPR001881; EGF_Ca_-trypsin.
InterPro; IPR006209; EGF_like.
InterPro; IPR002383; GLA_blood.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase S1A.
InterPro; IPR000294; VitK_dep_GLA.
Pfam; PF00008; EGF; 2.
Pfam; PF00594; gla; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PRO0722; CHYMOTRYPSIN.
PRINTS; PRO0001; GLABLOOD.
SMART; SM00179; EGF_CA; 1.
SMART; SM00069; GLA; 1.
SMART; SM00020; Tryp_Spc; 1.
PROSITE; PS00010; ASX_HYDROXYL; 1.
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS00026; EGF_3; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS00011; GLU_CARBOXYLATION; 1.
PROSITE; PS02040; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Blood coagulation; Glycoprotein; Serine protease;
Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
SIGNAL 1 32
PROPEP 33 41
CHAIN 42 196
CHAIN 199 461
PEPTIDE 199 212
SITE 212 213
DOMAIN 96 131
DOMAIN 135 175
DOMAIN 213 461
MOD_RES 47 47
MOD_RES 48 48
MOD_RES 55 55
MOD_RES 57 57
MOD_RES 60 60
MOD_RES 61 61
MOD_RES 66 66
MOD_RES 67 67
MOD_RES 70 70
MOD_RES 112 112
MOD_RES 254 254
ACT_SITE 300 300
ACT_SITE 402 402
DISULFID 58 63
DISULFID 91 110
DISULFID 100 105
DISULFID 104 119
DISULFID 121 130
DISULFID 139 150

CC modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announcement> or send an email to license@isb-sib.ch).

EMBL; X64336; CAA45617.1; -
FIR; S18994; S18994.
MEROPS; S01.218; -
InterPro; IPR000152; Asx hydroxyl S.
InterPro; IPR009003; Cys_ser_trypsin.
InterPro; IPR001881; EGF_Ca_-trypsin.
InterPro; IPR006209; EGF_like.
InterPro; IPR002383; GLA_blood.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase S1A.
InterPro; IPR000294; VitK_dep_GLA.
Pfam; PF00008; EGF; 2.
Pfam; PF00594; gla; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PRO0722; CHYMOTRYPSIN.
PRINTS; PRO0001; GLABLOOD.
SMART; SM00179; EGF_CA; 1.
SMART; SM00069; GLA; 1.
SMART; SM00020; Tryp_Spc; 1.
PROSITE; PS00010; ASX_HYDROXYL; 1.
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS00026; EGF_3; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS00011; GLU_CARBOXYLATION; 1.
PROSITE; PS02040; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Blood coagulation; Glycoprotein; Serine protease;
Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
SIGNAL 1 32
PROPEP 33 41
CHAIN 42 196
CHAIN 199 461
PEPTIDE 199 212
SITE 212 213
DOMAIN 96 131
DOMAIN 135 175
DOMAIN 213 461
MOD_RES 47 47
MOD_RES 48 48
MOD_RES 55 55
MOD_RES 57 57
MOD_RES 60 60
MOD_RES 61 61
MOD_RES 66 66
MOD_RES 67 67
MOD_RES 70 70
MOD_RES 112 112
MOD_RES 254 254
ACT_SITE 300 300
ACT_SITE 402 402
DISULFID 58 63
DISULFID 91 110
DISULFID 100 105
DISULFID 104 119
DISULFID 121 130
DISULFID 139 150

CC modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announcement> or send an email to <


```

FT DISULFID 396 424 BY SIMILARITY.
FT CARBOHYD 138 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 459 AA; 51866 MW; 8541AAC14CCL16D09 CRC64;

Query Match 62.4%; Score 123; DB 1; Length 459;
Best Local Similarity 52.3%; Pred. No. 5.4e-13;
Matches 23; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 1 ANSFLXLRGSLXRCIXXICDFFXAKXIFEDVDDTLAWSGH 44
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 42 ANSFLLELPSSLERECKTCTDFEARIFQNTMTAFWSKY 85

RESULT 6
PRTC_BOVIN STANDARD; PRT; 456 AA.
AC P00745;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Vitamin-K-dependent protein C precursor (PC 3, 4, 21-69)
DE (Antithrombin IIIA) (Anticoagulant protein C) (Blood coagulation
DE factor XIV) (Fragment).
GN PROC.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014826; PubMed=6091100;
RA Long G.L., Balagaje R.M., McGillivray R.T.A.;
RT "Cloning and sequencing of liver cDNA coding for bovine protein C.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5653-5656(1984).
RN [2]
RP SEQUENCE OF 40-194, AND CARBOHYDRATE-LINKAGE SITE ASN-136.
RX MEDLINE=83007325; PubMed=6896876;
RA Fernlund P., Stenflo J.;
RT "Amino acid sequence of the light chain of bovine protein C.";
RL J. Biol. Chem. 257:12170-12179(1982).
RN [3]
RP REVISION TO 110.
RX MEDLINE=83169769; PubMed=6572939;
RA Drakenberg T., Fernlund P., Roepstorff P., Stenflo J.;
RT "Beta-hydroxyaspartic acid in vitamin K-dependent protein C.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:1802-1806(1983).
RN [4]
RP SEQUENCE OF 197-456, AND CARBOHYDRATE-LINKAGE SITES ASN-289; ASN-350
RX AND ASN-366.
RX MEDLINE=83007326; PubMed=6896877;
RA Stenflo J., Fernlund P.;
RT "Amino acid sequence of the heavy chain of bovine protein C.";
RL J. Biol. Chem. 257:12180-12190(1982).
RN [5]
RP PROCESSING, AND CALCIUM-BINDING DATA.
RX MEDLINE=83213513; PubMed=6304032;
RA Esmon N.L., Debault L.E., Esmon C.T.;
RT "Proteolytic formation and properties of gamma-carboxyglutamic acid-
RT domainless protein C.";
RL J. Biol. Chem. 258:5548-5553(1983).
RN [6]
RP PROCESSING, AND CALCIUM-BINDING DATA.
RX MEDLINE=83213514; PubMed=6406503;
RA Johnson A.E., Esmon N.L., Laue T.M., Esmon C.T.;
RT "Structural changes required for activation of protein C are induced
RT by Ca2+ binding to a high affinity site that does not contain gamma-
RT carboxyglutamic acid.";
RL J. Biol. Chem. 258:5554-5560(1983).
CC -!- FUNCTION: Protein C is a vitamin K-dependent serine protease that
    regulates blood coagulation by inactivating factors Va and VIIIa

```

```

CC in the presence of calcium ions and phospholipids.
CC -!- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIIa.
CC -!- SUBUNIT: Synthesized as a single chain precursor, which is cleaved
CC into a light chain and a heavy chain held together by a disulfide
CC bond. The enzyme is then activated by thrombin, which cleaves a
CC tetradecapeptide from the amino end of the heavy chain; this
CC reaction, which occurs at the surface of endothelial cells, is
CC strongly promoted by thrombomodulin.
CC -!- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
CC -!- PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu
CC residues allows the modified protein to bind calcium.
CC -!- MISCELLANEOUS: Calcium also binds, with stronger affinity to
CC another site, beyond the GLA domain. This GLA-independent binding
CC site is necessary for the recognition of the thrombin-
CC thrombomodulin complex.
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- SIMILARITY: Contains 2 EGF-like domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; K02435; AAA30685.1; -.
CC PIR; A26250; KXEO.
CC HSRP; P04070; LPCU.
CC MEROPS; S01.218; -.
CC InterPro; IPR000152; Asx_hydroxyl_S.
CC InterPro; IPR009003; Cys_Ser_trypsin.
CC InterPro; IPR001881; EGF_Ca.
CC InterPro; IPR006209; EGF_Like.
CC InterPro; IPR002383; GLA_blood.
CC InterPro; IPR006210; IEGF.
CC InterPro; IPR001254; Peptidase_S1.
CC InterPro; IPR001314; Peptidase_S1A.
CC InterPro; IPR000294; VitK_dep_GLA.
CC Pfam; PF00008; EGF_2.
CC Pfam; PF00594; Gla_1.
CC Pfam; PF00083; tryptsin; 1.
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC PRINTS; PR00001; GLABLOOD.
CC SMART; SM00181; EGF_2.
CC SMART; SM00069; GLA; 1.
CC SMART; SM00020; Tryp_Spc; 1.
CC PROSITE; PS00010; ASX_HYDROXYL; 1.
CC PROSITE; PS00022; EGF_1; 1.
CC PROSITE; PS01186; EGF_2; 2.
CC PROSITE; PS00026; EGF_3; 1.
CC PROSITE; PS01187; EGF_CA; 1.
CC PROSITE; PS00011; GLU_CARBOXYLATION; 1.
CC PROSITE; PS02040; TRYPSIN_DOM; 1.
CC PROSITE; PS00134; TRYPSIN_HIS; FALSE_NEG.
CC PROSITE; PS00135; TRYPSIN_SER; 1.
CC Blood coagulation; Glycoprotein; Serine protease;
CC Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
CC EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
CC NON_TER 1 1
CC SIGNAL <1 29
CC PROPEP 30 39
CC CHAIN 40 194
CC CHAIN 197 456
CC PEPTIDE 197 210
CC DOMAIN 94 129
CC DOMAIN 133 173
CC DOMAIN 211 456
CC MOD_RES 45 45
CC MOD_RES 46 46
CC MOD_RES 53 53
CC MOD_RES 55 55
CC PROTEIN C LIGHT CHAIN.
CC PROTEIN C HEAVY CHAIN.
CC ACTIVATION PEPTIDE.
CC EGF-Like 1.
CC EGF-Like 2.
CC SERINE PROTEASE.
CC GAMMA-CARBOXYGLUTAMIC ACID.
CC GAMMA-CARBOXYGLUTAMIC ACID.
CC GAMMA-CARBOXYGLUTAMIC ACID.

```

```

FT MOD RES 58 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD RES 59 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD RES 62 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD RES 64 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD RES 65 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD RES 68 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD RES 74 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD RES 110 HYDROXYLATION.
FT ACT SITE 252 CHARGE RELAY SYSTEM.
FT ACT SITE 298 CHARGE RELAY SYSTEM.
FT ACT SITE 397 CHARGE RELAY SYSTEM.
FT DISULFID 56 BY SIMILARITY.
FT DISULFID 89 BY SIMILARITY.
FT DISULFID 98 BY SIMILARITY.
FT DISULFID 102 BY SIMILARITY.
FT DISULFID 119 BY SIMILARITY.
FT DISULFID 137 BY SIMILARITY.
FT DISULFID 144 BY SIMILARITY.
FT DISULFID 159 BY SIMILARITY.
FT DISULFID 180 INTERCHAIN.
FT DISULFID 237
FT DISULFID 238
FT DISULFID 368
FT DISULFID 393
FT CARBOHYD 136 N-LINKED (GLCNAC. . .)
FT CARBOHYD 289 N-LINKED (GLCNAC. . .)
FT CARBOHYD 350 N-LINKED (GLCNAC. . .)
FT CARBOHYD 366 F -> K.
FT VARIANT 82 VP -> PV (IN REF. 4).
FT CONFLICT 455
SQ SEQUENCE 456 AA; 51407 MW; CAAF6833F894C209 CRC64;

Query Match 61.9%; Score 122; DB 1; Length 456;
Best Local Similarity 50.0%; Pred. No. 7.9e-13;
Matches 21; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANSFLXLRQSLRXRTXICDFXXAKXIFEDVDDTLAFWS 42
DB 40 ANSFLXLRQSLRXRTXICDFXXAKXIFEDVDDTLAFWS 81

RESULT 7
FA10_BOVIN STANDARD; PRT; 492 AA.
AC P00743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
GN F10.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE OF 1-487 FROM N.A.
RX MEDLINE=84247315; PubMed=6330671;
RA Fung M.R., Campbell R.M., McGillicray R.T.A.;
RT "Blood coagulation factor X mRNA encodes a single polypeptide chain
RT containing a propro leader sequence."
RL Nucleic Acids Res. 12:4481-4492(1984).
RN [2]
RP SEQUENCE OF 41-180.
RX MEDLINE=80130563; PubMed=6766735;
RA Enfield D.L., Ericsson L.H., Fujikawa K., Walsh K.A., Neurath H.,
RA Titani K.;
RT "Amino acid sequence of the light chain of bovine factor XI (Stuart
RT factor).";
RL Biochemistry 19:659-667(1980).
RN [3]
RP REVISION TO 103.
RX MEDLINE=83308813; PubMed=6688526;
RA McMullen B.A., Fujikawa K., Kistel W.;

```

```

RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
RT k-dependent blood coagulation zymogens."
RL Biochem. Biophys. Res. Commun. 115:8-14(1983).
RN [4]
RP SEQUENCE OF 183-492, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
RX MEDLINE=76053069; PubMed=1059093;
RA Titani K., Fujikawa K., Enfield D.L., Ericsson L.H., Walsh K.A.,
RA Neurath H.;
RT "Bovine factor XI (Stuart factor): amino-acid sequence of heavy
RT chain."
RL Proc. Natl. Acad. Sci. U.S.A. 72:3082-3086(1975).
RN [5]
RP SEQUENCE OF 183-233, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=94062825; PubMed=8243451;
RA Inoue K., Morita T.;
RT "Identification of O-linked oligosaccharide chains in the activation
RT peptides of blood coagulation factor X. The role of the carbohydrate
RT moieties in the activation of factor X."
RL Eur. J. Biochem. 218:153-163(1993).
RN [6]
RP ACTIVE SITE.
RX MEDLINE=73053114; PubMed=4264286;
RA Titani K., Hermodsen M.A., Fujikawa K., Ericsson L.H., Walsh K.A.,
RA Neurath H., Davie E.W.;
RT "Bovine factor X 1a (activated Stuart factor). Evidence of homology
RT with mammalian serine proteases."
RL Biochemistry 11:4899-4903(1972).
RN [7]
RP PROCESSING.
RX MEDLINE=76053121; PubMed=1059122;
RA Fujikawa K., Titani K., Davie E.W.;
RT "Activation of bovine factor X (Stuart factor): conversion of factor
RT Xa-alpha to factor Xa-beta."
RL Proc. Natl. Acad. Sci. U.S.A. 72:3359-3363(1975).
RN [8]
RP CALCIUM-BINDING DATA.
RX MEDLINE=84185716; PubMed=6546930;
RA Sugo T., Bjorker I., Holmgren A., Stenflo J.;
RT "Calcium-binding properties of bovine factor X lacking the gamma-
RT carboxyglutamic acid-containing region."
RL J. Biol. Chem. 259:5705-5710(1984).
RN [9]
RP SULFATION.
RX MEDLINE=86140210; PubMed=3949800;
RA Morita T., Jackson C.M.;
RT "Localization of the structural difference between bovine blood
RT coagulation factors XI and X2 to tyrosine 18 in the activation
RT peptide."
RL J. Biol. Chem. 261:4008-4014(1986).
RN [10]
RP STRUCTURE BY NMR OF 85-126.
RX MEDLINE=91084483; PubMed=2261466;
RA Selander M., Persson E., Stenflo J., Drakenberg T.;
RT "1H NMR assignment and secondary structure of the Ca2(+)-free form of
RT the amino-terminal epidermal growth factor like domain in coagulation
RT factor X."
RL Biochemistry 29:8111-8118(1990).
RN [11]
RP STRUCTURE BY NMR OF 85-126.
RX MEDLINE=92329412; PubMed=1627540;
RA Ullner M., Selander M., Persson E., Stenflo J., Drakenberg T.,
RA Teleman O.;
RT "Three-dimensional structure of the apo form of the N-terminal
RT EGF-like module of blood coagulation factor X as determined by NMR
RT spectroscopy and simulated folding."
RL Biochemistry 31:5974-5983(1992).
RN [12]
RP STRUCTURE BY NMR OF 85-126.
RX MEDLINE=92406922; PubMed=1527084;
RA Selander-Sunnerhagen M., Ullner M., Persson E., Teleman O.,
RA Stenflo J., Drakenberg T.;
RT "How an epidermal growth factor (EGF)-like domain binds calcium. High
RT resolution NMR structure of the calcium form of the NH2-terminal EGF-

```

RT like domain in coagulation factor X."; J. Biol. Chem. 267:19642-19649(1992). [13]

RN STRUCTURE BY NMR OF 41-126.

RX MEDLINE=96387194; PubMed=8794734; Sunnerhagen M., Olah G.A., Stenflo J., Forsen S., Drakenberg T., Trewhella J.;

RA "The relative orientation of Gla and EGF domains in coagulation factor X is altered by Ca²⁺ binding to the first EGF domain. A combined NMR-small angle X-ray scattering study.";

RT Biochemistry 35:11347-11359(1996).

RL CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that converts prothrombin to thrombin in the presence of factor Va, calcium and phospholipid during blood clotting.

CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then Arg-|-Ile bonds in prothrombin to form thrombin.

CC -1- SUBUNIT: The two chains are formed from a single-chain precursor by the exclusion of two Arg residues and are held together by 1 or more disulfide bonds.

CC -1- PTM: The vitamin K-dependent, enzymatic carboxylation of some glutamate residues allows the modified protein to bind calcium.

CC -1- PTM: N- and O-glycosylated.

CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).

CC -1- MISCELLANEOUS: Calcium also binds, with stronger affinity to another site, beyond the GLA domain.

CC -1- SIMILARITY: Belongs to peptidase family S1.

CC -1- SIMILARITY: Contains 2 EGF-like domains.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

DR EMBL; X00673; CAZ5286.1; --

DR FIR; A22867; EXBO.

DR PDB; 1AFO; 31-JAN-94.

DR PDB; 1CCF; 31-MAY-94.

DR PDB; 1WHE; 15-MAY-97.

DR PDB; 1WHF; 15-MAY-97.

DR PDB; 1IOD; 21-JAN-03.

DR PDB; 1KIG; 28-OCT-98.

DR MEROPS; S01.216; --

DR GlycoSuiteDB; PC0743; --

DR InterPro; IPR000152; Asx_hydroxyl_S.

DR InterPro; IPR009003; Cys_ser_trypsin.

DR InterPro; IPR000742; EGF_2.

DR InterPro; IPR001881; EGF_Ca.

DR InterPro; IPR006209; EGF_like.

DR InterPro; IPR002383; GLA_blood.

DR InterPro; IPR001254; Peptidase_S1.

DR InterPro; IPR001314; Peptidase_S1A.

DR InterPro; IPR000294; VitK_dep_GLA.

DR Pfam; PR00008; EGF_2.

DR Pfam; PR00594; Gla; 1.

DR Pfam; PR00089; trypsin; 1.

DR PRINTS; PR00722; CHYNOTRYPsin.

DR PRINTS; PR00001; GLABLOOD.

DR SMART; SM00179; EGF_CA; 1.

DR SMART; SM00069; GLA; 1.

DR SMART; SM00020; TRYD_SPG; 1.

DR PROSITE; PS00010; ASX_HYDROXYL; 1.

DR PROSITE; PS00022; EGF_1; 1.

DR PROSITE; PS01186; EGF_2; 2.

DR PROSITE; PS00026; EGF_3; 1.

DR PROSITE; PS01187; EGF_CA; 1.

DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.

DR PROSITE; PS00240; TRYPSIN_DOM; 1.

DR PROSITE; PS00334; TRYPSIN_HIS; 1.

DR PROSITE; PS00135; TRYPSIN_SER; 1.

KW Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation; Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K; Signal; Zymogen; EGF-like domain; Repeat; Sulfation; 3D-structure. POTENTIAL.

FT SIGNAL 1 23

FT PROPEP 24 40

FT CHAIN 41 180

FT CHAIN 183 492

FT PROPEP 183 233

FT CHAIN 234 492

FT PROPEP 476 492

FT DOMAIN 86 122

FT DOMAIN 125 165

FT DOMAIN 234 492

FT ACT_SITE 275 275

FT ACT_SITE 321 321

FT ACT_SITE 418 418

FT MOD_RES 46 46

FT MOD_RES 47 47

FT MOD_RES 54 54

FT MOD_RES 56 56

FT MOD_RES 59 59

FT MOD_RES 60 60

Query Match 57.9%; Score 114; DB 1; Length 492;

Best Local Similarity 45.5%; Pred. No. 2e-11; Mismatches 16; Indels 0; Gaps 0;

Matches 20; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

KY 1 ANSFLLXLRQSLRXRXIXICDPXAKXIFEDVDDTLAFWSKH 44

DB 41 ANSFLEBYKGNLEECLEACSLSEAEVFEAEQTFDEFSKY 84

RESULT 8

FA10_HUMAN

ID FA10_HUMAN STANDARD; PRT; 488 AA.

AC P00742; Q14340;

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-OCT-1989 (Rel. 12, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).

GN F10.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=91216473; PubMed=1902434;

RA Messier T.L., Pittman D.D., Long G.L., Kaufman R.J., Church W.R.;

RT "Cloning and expression in COS-1 cells of a full-length cDNA encoding

human coagulation factor X.";

RL Gene 99:291-294(1991).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=87026600; PubMed=3769336;

RA Leytus S.P., Foster D.C., Kurachi K., Davie E.W.;

RT "Gene for human factor X: a blood coagulation factor whose gene

organization is essentially identical with that of factor IX and

protein C.";

RL Biochemistry 25:5098-5102(1986).

RN [3]

RP SEQUENCE FROM N.A.

RX Rieder M.J., Armel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,

RA Ozuna M., Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;

RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RX TISSUE-Ovary;

RA MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Narusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.D., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Woxley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villallon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinnwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences".
EL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RN SEQUENCE OF 13-488 FROM N.A.
RP MEDLINE=85216545; PubMed=2582420;
RX Fung M.R., Hay C.W., McGillivray R.T.A.;
RA "Characterization of an almost full-length cDNA coding for human
RT blood coagulation factor X".
EL Proc. Natl. Acad. Sci. U.S.A. 82:3591-3595(1985).
RN [6]
RN SEQUENCE OF 19-488 FROM N.A.
RP TISSUE=Liver;
RX MEDLINE=86221713; PubMed=3011603;
RA Kaul R.K., Hildebrand B., Roberts S., Jagadeeswaran P.;
RT "Isolation and characterization of human blood-coagulation factor X
RT cDNA".
EL Gene 41:311-314(1986).
RN [7]
RN SEQUENCE OF 41-179.
RX MEDLINE=93257207; PubMed=6871167;
RA McMullen B.A., Fujikawa K., Kisiel W., Sasagawa T., Howald W.N.,
RA Kwa E.Y., Weinstein B.;
RT "Complete amino acid sequence of the light chain of human blood
RT coagulation factor X: evidence for identification of residue 63 as
RT beta-hydroxyaspartic acid".
EL Biochemistry 22:2875-2884(1983).
RN [8]
RN SEQUENCE OF 115-488 FROM N.A., AND TISSUE SPECIFICITY.
RP TISSUE=Liver;
RX MEDLINE=94222026; PubMed=6587384;
RA Leytus S.P., Chung D.W., Kisiel W., Kurachi K., Davie E.W.;
RT "Characterization of a cDNA coding for human factor X".
EL Proc. Natl. Acad. Sci. U.S.A. 81:3699-3702(1984).
RN [9]
RN SEQUENCE OF 183-234, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=94062825; PubMed=8243461;
RA Inoue K., Morita T.;
RT "Identification of O-linked oligosaccharide chains in the activation
RT peptides of blood coagulation factor X. The role of the carbohydrate
RT moieties in the activation of factor X".
EL Eur. J. Biochem. 218:153-163(1993).
RN [10]
RN SEQUENCE OF 1-23 FROM N.A.
RX MEDLINE=90128299; PubMed=2612918;
RA Jagadeeswaran P., Reddy S.V., Rao K.J., Hamsabhusanam K., Lyman G.;
RT "Cloning and characterization of the 5' end (exon 1) of the gene
RT encoding human factor X".
EL Gene 84:517-519(1989).
RN [11]
RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 86-179 AND 235-278.
RX MEDLINE=93360277; PubMed=835279;
RA Padmanabhan K., Padmanabhan K.P., Tulinsky A., Park C.H., Bode W.,
RA Huber R., Blankenship D.T., Cardin A.D., Kisiel W.;
RT "Structure of human des(1-45) factor Xa at 2.2-A resolution".
EL J. Mol. Biol. 232:947-966(1993).
RN [12]
RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.
RX MEDLINE=98283982; PubMed=9618463;
RA Kamata K., Kawamoto H., Honma T., Iwama T., Kim S.H.;
RT "Structural basis for chemical inhibition of human blood coagulation
RT factor Xa".
EL Proc. Natl. Acad. Sci. U.S.A. 95:6630-6635(1998).
RN [13]
RN VARIANTS ILE-7 AND HIS-30.
RX MEDLINE=99318093; PubMed=10391209;
RA Cargill M., Altschuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
RA Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,
RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
RA Lander E.S.;
RT "Characterization of single-nucleotide polymorphisms in coding regions
RT of human genes".
EL Nat. Genet. 22:231-238(1999).
RN [14]
RN ERRATUM.
RP Cargill M., Altschuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
RA Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,
RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
RA Lander E.S.;
RT "FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
RT converts prothrombin to thrombin in the presence of factor Va,
RT calcium and phospholipid during blood clotting."
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
CC Arg-|-Ile bonds in prothrombin to form thrombin.
CC -!- SUBUNIT: The two chains are formed from a single-chain precursor
CC by the excision of two Arg residues and are held together by 1 or
CC more disulfide bonds.
CC -!- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
CC -!- PTM: The vitamin K-dependent, enzymatic carboxylation of some
CC glutamate residues allows the modified protein to bind calcium.
CC -!- PTM: N- and O-glycosylated.
CC -!- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- SIMILARITY: Contains 2 EGF-like domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)
CC or send an email to license@isb-sib.ch).
DR EMBL; K03194; AAA52490.1; -
DR EMBL; M57285; AAA52421.1; -
DR EMBL; AF503510; AM19347.1; -
DR EMBL; BC046125; AAH46125.1; -
DR EMBL; L29433; AAA52764.1; -
DR EMBL; L00390; AAA52764.1; JOINED.
DR EMBL; L00391; AAA52764.1; JOINED.
DR EMBL; L00392; AAA52764.1; JOINED.
DR EMBL; L00393; AAA52764.1; JOINED.
DR EMBL; L00394; AAA52764.1; JOINED.
DR EMBL; L00395; AAA52764.1; JOINED.
DR EMBL; L00396; AAA52764.1; JOINED.
DR EMBL; M22613; AAA51984.1; -
DR EMBL; K01886; AAA52486.1; -
DR EMBL; M33297; AAA52636.1; -
DR PIR; A24478; EXHU.
DR PDB; 1HCG; 08-MAY-95.
DR PDB; 1FAF; 23-OCT-97.
DR PDB; 1FXV; 17-JUN-98.
DR PDB; 1XKA; 23-MAR-99.
DR PDB; 1XKB; 23-MAR-99.
DR PDB; 1EZO; 20-SEP-00.
DR PDB; 1F08; 20-SEP-00.
DR PDB; 1F0S; 20-SEP-00.
DR PDB; 1FUS; 17-NOV-00.
DR PDB; 1G2L; 20-OCT-01.
DR PDB; 1G2M; 20-OCT-01.

InterPro; IPR001254; Peptidase S1.
 InterPro; IPR001314; Peptidase-S1A.
 InterPro; IPR000294; VICK_dep_GLA.
 Pfam; PF00008; EGF_2.
 Pfam; PF00594; Gla; 1.
 PRINTS; PRO0089; trypsin; 1.
 PRINTS; PRO0722; CHYMOTRYPSIN.
 PRINTS; PRO0010; EGFBLDOD.
 PRINTS; PRO0001; GLABLOOD.
 SMART; SM00179; EGF_CA; 1.
 SMART; SM00069; GLA; 1.
 SMART; SM00020; Tryp_Spc; 1.
 PROSITE; PS00010; ASX_HYDROXYL; 1.
 PROSITE; PS00022; EGF_1; 1.
 PROSITE; PS01186; EGF_2; 2.
 PROSITE; PS00026; EGF_3; 1.
 PROSITE; PS01187; EGF_CA; 1.
 PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 PROSITE; PS02040; TRYPSIN_DOM; 1.
 PROSITE; PS00134; TRYPSIN_HIS; 1.
 PROSITE; PS00135; TRYPSIN_SER; 1.
 Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;
 Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
 Signal; Zymogen; EGF-like domain; Repeat.
 SIGNAL 1 20
 PROPEP 21 40
 CHAIN 41 180
 CHAIN 184 490
 PROPEP 184 232
 CHAIN 233 490
 DOMAIN 86 122
 DOMAIN 125 165
 DOMAIN 233 490
 MOD_RES 46 46
 MOD_RES 47 47
 MOD_RES 54 54
 MOD_RES 56 56
 MOD_RES 59 59
 MOD_RES 60 60
 MOD_RES 65 65
 MOD_RES 66 66
 MOD_RES 69 69
 MOD_RES 72 72
 MOD_RES 75 75
 MOD_RES 79 79
 MOD_RES 103 103
 ACT_SITE 274 274
 ACT_SITE 320 320
 ACT_SITE 417 417
 DISULFID 90 101
 DISULFID 95 110
 DISULFID 112 121
 DISULFID 129 140
 DISULFID 136 149
 DISULFID 151 164
 DISULFID 172 340
 DISULFID 239 244
 DISULFID 259 275
 DISULFID 388 402
 DISULFID 413 441
 CARBOHYD 61 61

InterPro; IPR001254; Peptidase S1.
 InterPro; IPR001314; Peptidase-S1A.
 InterPro; IPR000294; VICK_dep_GLA.
 Pfam; PF00008; EGF_2.
 Pfam; PF00594; Gla; 1.
 PRINTS; PRO0089; trypsin; 1.
 PRINTS; PRO0722; CHYMOTRYPSIN.
 PRINTS; PRO0010; EGFBLDOD.
 PRINTS; PRO0001; GLABLOOD.
 SMART; SM00179; EGF_CA; 1.
 SMART; SM00069; GLA; 1.
 SMART; SM00020; Tryp_Spc; 1.
 PROSITE; PS00010; ASX_HYDROXYL; 1.
 PROSITE; PS00022; EGF_1; 1.
 PROSITE; PS01186; EGF_2; 2.
 PROSITE; PS00026; EGF_3; 1.
 PROSITE; PS01187; EGF_CA; 1.
 PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 PROSITE; PS02040; TRYPSIN_DOM; 1.
 PROSITE; PS00134; TRYPSIN_HIS; 1.
 PROSITE; PS00135; TRYPSIN_SER; 1.
 Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;
 Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
 Signal; Zymogen; EGF-like domain; Repeat.
 SIGNAL 1 20
 PROPEP 21 40
 CHAIN 41 180
 CHAIN 184 490
 PROPEP 184 232
 CHAIN 233 490
 DOMAIN 86 122
 DOMAIN 125 165
 DOMAIN 233 490
 MOD_RES 46 46
 MOD_RES 47 47
 MOD_RES 54 54
 MOD_RES 56 56
 MOD_RES 59 59
 MOD_RES 60 60
 MOD_RES 65 65
 MOD_RES 66 66
 MOD_RES 69 69
 MOD_RES 72 72
 MOD_RES 75 75
 MOD_RES 79 79
 MOD_RES 103 103
 ACT_SITE 274 274
 ACT_SITE 320 320
 ACT_SITE 417 417
 DISULFID 90 101
 DISULFID 95 110
 DISULFID 112 121
 DISULFID 129 140
 DISULFID 136 149
 DISULFID 151 164
 DISULFID 172 340
 DISULFID 239 244
 DISULFID 259 275
 DISULFID 388 402
 DISULFID 413 441
 CARBOHYD 61 61

InterPro; IPR001254; Peptidase S1.
 InterPro; IPR001314; Peptidase-S1A.
 InterPro; IPR000294; VICK_dep_GLA.
 Pfam; PF00008; EGF_2.
 Pfam; PF00594; Gla; 1.
 PRINTS; PRO0089; trypsin; 1.
 PRINTS; PRO0722; CHYMOTRYPSIN.
 PRINTS; PRO0010; EGFBLDOD.
 PRINTS; PRO0001; GLABLOOD.
 SMART; SM00179; EGF_CA; 1.
 SMART; SM00069; GLA; 1.
 SMART; SM00020; Tryp_Spc; 1.
 PROSITE; PS00010; ASX_HYDROXYL; 1.
 PROSITE; PS00022; EGF_1; 1.
 PROSITE; PS01186; EGF_2; 2.
 PROSITE; PS00026; EGF_3; 1.
 PROSITE; PS01187; EGF_CA; 1.
 PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 PROSITE; PS02040; TRYPSIN_DOM; 1.
 PROSITE; PS00134; TRYPSIN_HIS; 1.
 PROSITE; PS00135; TRYPSIN_SER; 1.
 Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;
 Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
 Signal; Zymogen; EGF-like domain; Repeat.
 SIGNAL 1 20
 PROPEP 21 40
 CHAIN 41 180
 CHAIN 184 490
 PROPEP 184 232
 CHAIN 233 490
 DOMAIN 86 122
 DOMAIN 125 165
 DOMAIN 233 490
 MOD_RES 46 46
 MOD_RES 47 47
 MOD_RES 54 54
 MOD_RES 56 56
 MOD_RES 59 59
 MOD_RES 60 60
 MOD_RES 65 65
 MOD_RES 66 66
 MOD_RES 69 69
 MOD_RES 72 72
 MOD_RES 75 75
 MOD_RES 79 79
 MOD_RES 103 103
 ACT_SITE 274 274
 ACT_SITE 320 320
 ACT_SITE 417 417
 DISULFID 90 101
 DISULFID 95 110
 DISULFID 112 121
 DISULFID 129 140
 DISULFID 136 149
 DISULFID 151 164
 DISULFID 172 340
 DISULFID 239 244
 DISULFID 259 275
 DISULFID 388 402
 DISULFID 413 441
 CARBOHYD 61 61

InterPro; IPR001254; Peptidase S1.
 InterPro; IPR001314; Peptidase-S1A.
 InterPro; IPR000294; VICK_dep_GLA.
 Pfam; PF00008; EGF_2.
 Pfam; PF00594; Gla; 1.
 PRINTS; PRO0089; trypsin; 1.
 PRINTS; PRO0722; CHYMOTRYPSIN.
 PRINTS; PRO0010; EGFBLDOD.
 PRINTS; PRO0001; GLABLOOD.
 SMART; SM00179; EGF_CA; 1.
 SMART; SM00069; GLA; 1.
 SMART; SM00020; Tryp_Spc; 1.
 PROSITE; PS00010; ASX_HYDROXYL; 1.
 PROSITE; PS00022; EGF_1; 1.
 PROSITE; PS01186; EGF_2; 2.
 PROSITE; PS00026; EGF_3; 1.
 PROSITE; PS01187; EGF_CA; 1.
 PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 PROSITE; PS02040; TRYPSIN_DOM; 1.
 PROSITE; PS00134; TRYPSIN_HIS; 1.
 PROSITE; PS00135; TRYPSIN_SER; 1.
 Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;
 Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
 Signal; Zymogen; EGF-like domain; Repeat.
 SIGNAL 1 20
 PROPEP 21 40
 CHAIN 41 180
 CHAIN 184 490
 PROPEP 184 232
 CHAIN 233 490
 DOMAIN 86 122
 DOMAIN 125 165
 DOMAIN 233 490
 MOD_RES 46 46
 MOD_RES 47 47
 MOD_RES 54 54
 MOD_RES 56 56
 MOD_RES 59 59
 MOD_RES 60 60
 MOD_RES 65 65
 MOD_RES 66 66
 MOD_RES 69 69
 MOD_RES 72 72
 MOD_RES 75 75
 MOD_RES 79 79
 MOD_RES 103 103
 ACT_SITE 274 274
 ACT_SITE 320 320
 ACT_SITE 417 417
 DISULFID 90 101
 DISULFID 95 110
 DISULFID 112 121
 DISULFID 129 140
 DISULFID 136 149
 DISULFID 151 164
 DISULFID 172 340
 DISULFID 239 244
 DISULFID 259 275
 DISULFID 388 402
 DISULFID 413 441
 CARBOHYD 61 61

InterPro; IPR001254; Peptidase S1.
 InterPro; IPR001314; Peptidase-S1A.
 InterPro; IPR000294; VICK_dep_GLA.
 Pfam; PF00008; EGF_2.
 Pfam; PF00594; Gla; 1.
 PRINTS; PRO0089; trypsin; 1.
 PRINTS; PRO0722; CHYMOTRYPSIN.
 PRINTS; PRO0010; EGFBLDOD.
 PRINTS; PRO0001; GLABLOOD.
 SMART; SM00179; EGF_CA; 1.
 SMART; SM00069; GLA; 1.
 SMART; SM00020; Tryp_Spc; 1.
 PROSITE; PS00010; ASX_HYDROXYL; 1.
 PROSITE; PS00022; EGF_1; 1.
 PROSITE; PS01186; EGF_2; 2.
 PROSITE; PS00026; EGF_3; 1.
 PROSITE; PS01187; EGF_CA; 1.
 PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 PROSITE; PS02040; TRYPSIN_DOM; 1.
 PROSITE; PS00134; TRYPSIN_HIS; 1.
 PROSITE; PS00135; TRYPSIN_SER; 1.
 Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;
 Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
 Signal; Zymogen; EGF-like domain; Repeat.
 SIGNAL 1 20
 PROPEP 21 40
 CHAIN 41 180
 CHAIN 184 490
 PROPEP 184 232
 CHAIN 233 490
 DOMAIN 86 122
 DOMAIN 125 165
 DOMAIN 233 490
 MOD_RES 46 46
 MOD_RES 47 47
 MOD_RES 54 54
 MOD_RES 56 56
 MOD_RES 59 59
 MOD_RES 60 60
 MOD_RES 65 65
 MOD_RES 66 66
 MOD_RES 69 69
 MOD_RES 72 72
 MOD_RES 75 75
 MOD_RES 79 79
 MOD_RES 103 103
 ACT_SITE 274 274
 ACT_SITE 320 320
 ACT_SITE 417 417
 DISULFID 90 101
 DISULFID 95 110
 DISULFID 112 121
 DISULFID 129 140
 DISULFID 136 149
 DISULFID 151 164
 DISULFID 172 340
 DISULFID 239 244
 DISULFID 259 275
 DISULFID 388 402
 DISULFID 413 441
 CARBOHYD 61 61

FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 490 AA; 53965 MW; 3A39FA85AF2A6D11 CRC64;
 Query Match 52.3%; Score 103; DB 1; Length 490;
 Best Local Similarity 43.2%; Pred No. 1.4e-09;
 Matches 19; Conservative 9; Mismatches 16; Indels 0; Gaps 0;
 QY 1 ANSFLXLRQGSIXXCIXXICDFXXAXXIFEDVDDTLAFWSKH 44
 DB 41 ANSFLEELKGNLERECMEENCYSBEALEVFEFDREKTNFVWKY 84
 RESULT 11
 PA7_RABIT
 ID PA7_RABIT STANDARD; PRT; 444 AA.
 AC P98139; P79224;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
 DE conversion accelerator).
 GN F7.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=93190306; PubMed=8383365;
 RA Brothers A.B., Clarke B.J., Sheffield W.P., Blajchman M.A.;
 RT "Complete nucleotide sequence of the cDNA encoding rabbit coagulation
 RT factor VII.";
 RL Thromb. Res. Suppl. 69:231-238(1993).
 RN [2]
 RP REVISION TO 395.
 RC TISSUE=Liver;
 RA Ruiz S.R., Blajchman M.A., Clarke B.J.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Circulates in the blood in a zymogen form. Factor VII is
 CC converted to factor VIIa by factor Xa, factor XIIa, factor IXa, or
 CC thrombin by minor proteolysis. In the presence of tissue factor
 CC and calcium ions, factor VIIa then converts factor X to factor Xa
 CC by limited proteolysis. Factor VIIa will also convert factor IX to
 CC factor IXa in the presence of tissue factor and calcium (By
 CC similarity).
 CC -!- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
 CC form factor Xa.
 CC -!- SUBUNIT: Heterodimer of a light chain and a heavy chain linked by
 CC a disulfide bond (By similarity).
 CC -!- TISSUE SPECIFICITY: Plasma.
 CC -!- PTM: The vitamin K-dependent, enzymatic carboxylation of some
 CC glutamate residues allows the modified protein to bind calcium (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to peptidase family S1.
 CC -!- SIMILARITY: Contains 2 EGF-like domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U77477; AAB37326.1; -;
 CC HSSP; P08709; 1FAK.
 CC MEROPS; S01.215; -;
 CC InterPro; IPR000152; Asx_hydroxyl_S.
 CC InterPro; IPR009003; Cys_Ser_trypsin.
 CC InterPro; IPR000742; EGF_2.
 CC InterPro; IPR001881; EGF_Ca.
 CC DR

RT first EGF-like domain of clotting factors VII and IX and protein Z.";
 RL Adv. Exp. Med. Biol. 281:121-131(1990).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
 RX MEDLINE=96175641; PubMed=8598903;
 RA Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,
 RA Konigsberg W.H., Nemerson Y., Kirchhofer D.,
 RT "The crystal structure of the complex of blood coagulation factor
 RT VIIa with soluble tissue factor.";
 RL Nature 380:41-46(1996).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
 RX MEDLINE=99126538; PubMed=925787;
 RA Zhang E., St Charles R., Tulinsky A.,
 RT "Structure of extracellular tissue factor complexed with factor VIIa
 RT inhibited with a BPTI mutant.";
 RL J. Mol. Biol. 285:2089-2104(1999).
 RN [10]
 RP STRUCTURE BY NMR OF 105-145.
 RX MEDLINE=98367502; PubMed=9692950;
 RA Muranyi A., Finn B.E., Gippert G.P., Forsen S., Stenflo J.,
 RA Drakenberg T.,
 RT "Solution structure of the N-terminal EGF-like domain from human
 RT factor VII.";
 RL Biochemistry 37:10605-10615(1998).
 RN [11]
 RP VARIANT GLN-364.
 RX MEDLINE=91300046; PubMed=2070047;
 RA O'Brien D.P., Gale K.M., Anderson J.S., McVey J.H., Miller G.J.,
 RA Meade T.W., Tuddenham E.G.D.,
 RT "Purification and characterization of factor VII 304-Gln: a variant
 RT molecule with reduced activity isolated from a clinically unaffected
 RT male.";
 RL Blood 78:132-140(1991).
 RN [12]
 RP VARIANTS GLN-364 AND PHE-370.
 RX MEDLINE=92340074; PubMed=1634227;
 RA Marchetti G., Patrachini P., Gemmati D., Derosa V., Pinotti M.,
 RA Rodorigo G., Casonato A., Girolami A., Bernardi F.,
 RT "Detection of two missense mutations and characterization of a repeat
 RT polymorphism in the factor VII gene (F7).";
 RL Hum. Genet. 89:497-502(1992).
 RN [13]
 RP VARIANT TYR-238.
 RX MEDLINE=93372811; PubMed=8364544;
 RA Marchetti G., Ferrati M., Patrachini P., Redaelli R., Bernardi F.,
 RT "A missense mutation (178Cys-->Tyr) and two neutral dimorphisms
 RT (115His and 333Ser) in the human coagulation factor VII Gene.";
 RL Hum. Mol. Genet. 2:1055-1056(1993).
 RN [14]
 RP VARIANTS.
 RX MEDLINE=94061028; PubMed=8242057;
 RA Takamiya O., Kemball-Cook G., Martin D.M.A., Cooper D.N.,
 RA von Felten A., Meili E., Hahn I., Pragnell D.R., Lumley H.,
 RA Tuddenham E.G.D., McVey J.H.,
 RT "Detection of missense mutations by single-strand conformational
 RT polymorphism (SSCP) analysis in five dysfunctional variants of
 RT coagulation factor VII.";
 RL Hum. Mol. Genet. 2:1355-1359(1993).
 RN [15]
 RP VARIANTS CHARLOTTE GLN-139 AND GLN-212.
 RX MEDLINE=94264305; PubMed=8204879;
 RA Chaing S., Clarke B., Sridhara S., Chu K., Friedman P., Vandusen W.,
 RA Roberts H.R., Blajchman M., Monroe D.M., High K.A.,
 RT "Severe factor VII deficiency caused by mutations abolishing the
 RT cleavage site for activation and altering binding to tissue factor.";
 RL Blood 83:3524-3535(1994).
 RN [16]
 RP VARIANT VAL-354.
 RX MEDLINE=95072589; PubMed=7981691;
 RA Bernardi F., Castaman G., Redaelli R., Pinotti M., Lunghi B.,
 RA Rodeghiero F., Marchetti G.,
 RT "Topologically equivalent mutations causing dysfunctional coagulation

RT factors VII (294Ala-->Val) and X (334Ser-->Pro).";
 RL Hum. Mol. Genet. 3:1175-1177(1994).
 RN [17]
 RP VARIANT MIE HIS-307.
 RX MEDLINE=95064662; PubMed=7974346;
 RA Ohiwa M., Hayashi T., Wada H., Minamikawa K., Shirakawa S.,
 RA Suzuki K.,
 RT "Factor VII MIE: homozygous asymptomatic type I deficiency caused by
 RT an amino acid substitution of His (CAC) for Arg(247) (CGC) in the
 RT catalytic domain.";
 RL Thromb. Haemost. 71:773-777(1994).
 RN [18]
 RP VARIANT MET-419.
 RX MEDLINE=96247510; PubMed=8652821;
 RA Arbini A.A., Mannucci P.M., Bader K.A.,
 RT "A Thr39Met mutation in factor VII of a patient with a hereditary
 RT deficiency causes defective secretion of the molecule.";
 RL Blood 87:5085-5094(1996).
 RN [19]
 RP VARIANTS TRP-283; LYS-325; VAL-358; GLN-364; GLU-402 AND GLN-413.
 RX MEDLINE=97001216; PubMed=8944208;
 RA Bernardi F., Castaman G., Pinotti M., Ferraresi P., di Iasio M.G.,
 RA Lunghi B., Rodeghiero F., Marchetti G.,
 RT "Mutation pattern in clinically asymptomatic coagulation factor VII
 RT deficiency.";
 RL Hum. Mutat. 8:108-115(1996).
 RN [20]
 RP VARIANT VAL-304.
 RX MEDLINE=97037613; PubMed=8883260;
 RA Tamary H., Fromovich Y., Shalom D., Reich Z., Dym O., Lanir N.,
 RA Brenner S., Paz M., Luder A.S., Blau O., Korostishevsky M.,
 RA Zaitov R., Seiligson U.,
 RT "Ala244Val is a common, probably ancient mutation causing factor VII
 RT deficiency in Moroccan and Iranian Jews.";
 RL Thromb. Haemost. 76:283-291(1996).
 RN [21]
 RP VARIANT MORIOKA PRO-13.
 RX MEDLINE=98235713; PubMed=9576180;
 RA Ozawa T., Takikawa Y., Niiya K., Ejiri N., Suzuki K., Sato S.,
 RA Sakuragawa N.,
 RT "Factor VII Moriooka (FVII L-26P): a homozygous missense mutation in
 RT the signal sequence identified in a patient with factor VII
 RT deficiency.";
 RL Br. J. Haematol. 101:47-49(1998).
 RN [22]
 RP VARIANTS MALTA THR-194 AND VAL-304.
 RX MEDLINE=98112461; PubMed=9452082;
 RA Alshinawi C., Scerri C., Galdies R., Aquilina A., Felice A.E.,
 RT "Two new missense mutations (P134T and A244V) in the coagulation
 RT factor VII gene.";
 RL Hum. Mutat. Suppl. 1:S189-S191(1998).
 RN [23]
 RP VARIANTS ASP-295 AND GLN-413.
 RX MEDLINE=99318093; PubMed=10391209;
 RA Cagill M., Altschuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
 RA Shaw N., Lane C.R., Lim E.P., Kalyanaram N., Nimesh J., Ziaugra L.,
 RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
 RA Lander E.S.,
 RT "Characterization of single-nucleotide polymorphisms in coding regions
 RT of human genes.";
 RL Nat. Genet. 22:231-238(1999).

Query Match 50.3%; Score 99; DB 1; Length 466;

Best Local Similarity 48.8%; Pred. No. 6:5e-09;

Matches 20; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 ANSPFLXKRGCSLXRXCIXXICDFXXAKXIFEDVDDTLAFW 41

DB 61 ANAPLELRPGSLERECKEQCSFEAREIFKDAERTKLEW 101

RESULT 13
 TWGI_HUMAN


```

DR SMART; SM00130; KR; 2.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
DR PROSITE; PS00021; KRINGLE_1; 2.
DR PROSITE; PS00070; KRINGLE_2; 2.
DR PROSITE; PS00240; TRYPsin_DOM; 1.
DR PROSITE; PS00134; TRYPsin_HIS; 1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
KW Blood coagulation; Plasma; Calcium-binding; Glycoprotein; Repeat;
KW Vitamin K; Zymogen; Gamma-carboxyglutamic acid; Acute phase; Liver;
KW Hydrolase; Serine protease; Kringle; Signal.
FT SIGNAL 1 24
FT PROPEP 25 43
FT CHAIN 44 617
FT PEPTIDE 44 200
FT PEPTIDE 201 323
FT CHAIN 324 359
FT CHAIN 360 617
FT DOMAIN 109 187
FT DOMAIN 215 292
FT DOMAIN 360 617
FT SITE 200 201
FT SITE 323 324
FT SITE 359 360
FT ACT_SITE 402 402
FT ACT_SITE 458 458
FT ACT_SITE 564 564
FT MOD_RES 50 50
FT MOD_RES 51 51
FT MOD_RES 58 58
FT MOD_RES 60 60
FT MOD_RES 63 63
FT MOD_RES 64 64
FT MOD_RES 69 69
FT MOD_RES 70 70
FT MOD_RES 73 73
FT MOD_RES 76 76
FT CARBOHYD 120 120
FT CARBOHYD 144 144
FT CARBOHYD 412 412
FT CARBOHYD 552 552
FT DISULFID 61 66
FT DISULFID 91 104
FT DISULFID 109 187
FT DISULFID 130 170
FT DISULFID 158 182
FT DISULFID 215 292
FT DISULFID 236 276
FT DISULFID 264 287
FT DISULFID 332 478
FT DISULFID 387 403
FT DISULFID 532 546
FT DISULFID 560 590
SQ SEQUENCE 617 AA; AD27DLB17445DB1D CRC64;

Query Match 43.9%; Score 86.5; DB 1; Length 617;
Best Local Similarity 42.2%; Pred. No. 1.2e-06;
Matches 19; Conservative 6; Mismatches 19; Indels 1; Gaps 1;

OY 1 ANS-FLKXLFQGSIXRXCIXXICDFXAXXIFPDVDDTLAFWSKH 44
DB 44 ANSGFLEELRKNGLRECEVQCSYEAFEALESQDQTVFWAKY 88

RESULT 15
THRB_MOUSE
ID THRB_MOUSE STANDARD; PRT; 618 AA.
AC P19221;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Prothrombin precursor (EC 3.4.21.5).
GN F2 OR CF2.

```

```

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Liver;
RX MEDLINE=91025551; PubMed=2222810;
RA Friesner Degen S.J., Schaffer L.A., Jamison C.S., Grant S.G.,
RA Fitzgibbon J.J., Fai J.-A., Chapman V.M., Elliott R.W.;
RT "Characterization of the cDNA coding for mouse prothrombin and
RT localization of the gene on mouse chromosome 2.";
RL DNA Cell Biol. 9:487-498(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Greenwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE OF 384-618 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=92212913; PubMed=1557383;
RA Banfield D.K., Macgillivray R.T.;
RT "partial characterization of vertebrate prothrombin cDNAs:
RT amplification and sequence analysis of the B chain of thrombin from
RT nine different species.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
CC -!- FUNCTION: Thrombin, which cleaves bonds after Arg and Lys,
CC converts fibrinogen to fibrin and activates factors V, VII, VIII,
CC XIII, and, in complex with thrombomodulin, protein C.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Gly; activates
CC fibrinogen to fibrin and releases fibrinopeptide A and B.
CC -!- PTM: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,
CC RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL
CC ENZYME, THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES
CC ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY
CC CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION
CC OF PROTHROMBIN TO THROMBIN.
CC -!- MISCELLANEOUS: Prothrombin is activated on the surface of a
CC phospholipid membrane that binds the amino end of prothrombin and
CC factors Va and Xa in Ca-dependent interactions; factor Xa removes
CC the activation peptide and cleaves the remaining part into light
CC and heavy chains. The activation process starts slowly because
CC factor V itself has to be activated by the initial, small amounts
CC of thrombin.
CC -!- MISCELLANEOUS: Thrombin can itself cleave the amino terminal
CC fragment (fragment 1) of the prothrombin, prior to its activation
CC by factor Xa.
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- SIMILARITY: Contains 2 kringle domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its

```

use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/>) or send an email to license@isb-sib.ch.

CC EMBL; X52308; CAA36548.1; .
CC EMBL; BC013662; AAI13662.1; .
CC EMBL; M81394; AAA40435.1; .
CC PIR; A35827; A35827.
CC HSP; P00734; 1B7X.
CC MEROPS; S01.217; .
CC MGD; MGI:88180; F2.
CC InterPro; IPR009003; Cys Ser trypsin.
CC InterPro; IPR002383; GLA blood.
CC InterPro; IPR000001; Kringle.
CC InterPro; IPR001254; Peptidase S1.
CC InterPro; IPR001314; Peptidase S1A.
CC InterPro; IPR003966; Peptidase S1A pr.
CC InterPro; IPR00294; VitK_dep_GLA.
CC Pfam; PF00594; Gla; 1.
CC Pfam; PF00051; kringle; 2.
CC Pfam; PF00089; trypsin; 1.
CC PRINTS; PRO0722; CHYMOTRYPSIN.
CC PRINTS; PRO0001; GLABLOOD.
CC PRINTS; PRO0018; KRINGLE.
CC PRINTS; PRO1505; PROTHROMBIN.
CC ProDom; PD000395; Kringle; 2.
CC SMART; SM00069; GLA; 1.
CC SMART; SM00130; KR; 2.
CC PROSITE; PS00020; Tryp SPC; 1.
CC PROSITE; PS00011; GLU CARBOXYLATION; 1.
CC PROSITE; PS00021; KRINGLE 1; 2.
CC PROSITE; PS00070; KRINGLE 2; 2.
CC PROSITE; PS00240; TRYPSIN_DOM; 1.
CC PROSITE; PS00134; TRYPSIN_HIS; 1.
CC PROSITE; PS00135; TRYPSIN_SER; 1.
KW Blood coagulation; Plasma; Calcium-binding; Glycoprotein; Repeat;
KW Vitamin K; Zymogen; Gamma-carboxyglutamic acid; Acute phase; Liver;
KW Hydroxylase; Serine protease; Kringle; Signal.
FT SIGNAL 1 24
FT PROPEP 25 43
FT CHAIN 44 618
FT PEPTIDE 44 200
FT PEPTIDE 201 324
FT CHAIN 325 360
FT CHAIN 361 618
FT DOMAIN 109 187
FT DOMAIN 215 292
FT DOMAIN 351 618
FT SITE 200 201
FT SITE 324 325
FT SITE 360 361
FT ACT_SITE 403 403
FT ACT_SITE 459 459
FT ACT_SITE 565 565
FT MOD_RES 50 50
FT MOD_RES 51 51
FT MOD_RES 58 58
FT MOD_RES 60 60
FT MOD_RES 63 63
FT MOD_RES 64 64
FT MOD_RES 69 69
FT MOD_RES 70 70
FT MOD_RES 73 73
FT MOD_RES 76 76
FT DISULFID 61 66
FT DISULFID 91 104
FT DISULFID 109 187
FT DISULFID 130 170
FT DISULFID 158 182
FT DISULFID 215 293
FT DISULFID 236 276
FT DISULFID 264 288

FT DISULFID 333 479 INTERCHAIN (BY SIMILARITY).
FT DISULFID 388 404 BY SIMILARITY.
FT DISULFID 533 547 BY SIMILARITY.
FT DISULFID 561 591 BY SIMILARITY.
FT CARBOHYD 122 122 N-LINKED (GLCNAC. . .).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .).
FT CARBOHYD 413 413 N-LINKED (GLCNAC. . .).
FT CARBOHYD 553 553 N-LINKED (GLCNAC. . .).
SQ SEQUENCE 618 AA; 70268 MW; 889P719AAF601E0 CRC64;
Query Match 43.98; Score 86.5; DB 1; Length 618;
Best Local Similarity 42.2%; Pred. No. 1.2e-06;
Matches 19; Conservative 6; Mismatches 19; Indels 1; Gaps 1;
QY 1 ANS-FLXLRQGSIXRCIXXICDFXAXKIFEDVDDTLAFWSKH 44
Db 44 ANSGFLEELRKGNLERECVEEQCSYEAFPALESPOQTDVFWAKY 88
Search completed: March 1, 2004, 10:03:23
Job time : 10.5 secs